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RESULT 5

OBKFB5 CHLTE
OBKFB5;

AC OBKFB5;

CHTEMBLrel. 22,
DT 01-OCT-2002 (TrEMBLrel. 22,
DT 01-OCT-2003 (TrEMBLrel. 25,
DT 01-OCT-2003 (TrEMBLrel. 22,
DT 01-OCT-203 (TREMBLRel. 22,
DT 01-OCT-20
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R EMBL; AE009247; AAL41996.1; -; Genomic_DNA.

R EMBL; AE008366; AAK90206.1; -; Genomic_DNA.

R PIR; AF2947; AF2947.

R PIR; D98315; D98335.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:001687; F:ATPasse activity; IEA.

R GO; GO:001687; F:MTPasse activity; IEA.

R GO; GO:0001687; F:MTPasse activity; IEA.
                                                                                                                                          NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SUPPRISED SEQUENCE.

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NUCLEOTIDE SUPPRISED SEQUENCE.

NUCLEOTIDE SEQUENCE.

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InterPro; IPR003439; ABC transp_like.
Pfam; PF00005; ABC trans; 1.
ProDom; PD000006; ABC transporter; 1.
SMART; SM00382; AAA; 1.
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Science
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Iron(III) ABC transporter, ATP-binding protein, put
OrderedLocusNames=CT0412;
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PROSITE; PS00211; ABC TRANSPORTER 1; UNKNOWN 1.

PROSITE; PS50893; ABC_TRANSPORTER 2; 1.

ATP-binding; Complete proteome; Nucleotide-bind SEQUENCE 277 AA; 29733 MW; 282D3AA83B0D9124
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                                                                           photosynthetic, anaerobic, green-sulfur bacterium."; Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
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29733 MW; 282D3AA83B0D9124 CRC64;
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016887; F:ATPase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR003593; AAA_ATPase.
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InterPro; IPR003593; ABC_transp_like.
InterPro; IPR003439; ABC_tran; 1.
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PubMed=15383718; DOI=10.1159/000079829;

PubMed=15383718; DOI=10.1159/000079829;

Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,

Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,

Ehrenreich A., Gottschalk G.;

"The complete genome sequence of Bacillus licheniformis DSM13,

organism with great industrial potential.";

J., Mol. Microbiol. Biotechnol. 7:204-211(2004).
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ProDom; PD000006; ABC 1
SMART; SM00382; AAA; 1
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                                                                                                                                                                                                                                 "Complete genome sequence of the industrial bacterium Bacillus licheniformis and comparisons with closely related Bacillus specerome Biol. 5:RESEARCH077.1-RESEARCH077.12 (2004).

EMBL; AE017333; AAU42873.1; -; Genomic_DNA.

EMBL; CP000002; AAU25501.1; -; Genomic_DNA.

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf.
                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=15461803; DOI=10.1186/gb-2004-5-10-r77; Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Z Tang M., Lopez de Leon A., Xiang H., Gusti V., Clausen Olsen P.B., Rasmussen M.D., Andeersen J.T., Joergensen P Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galler Ehrlich S.D., Berka R.M.;
                                                                                                                                      InterPro; IPR002478; PUA.
InterPro; IPR000051; SAM_bd.
SMART; SM00359; PUA; 1.
PROSITE; PS50890; PUA; 1.
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Pred. No.
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Pred.
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                                                Length 396;
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InterPro; IPR006210; IEGF.
InterPro; IPR001791; Laminin G.
InterPro; IPR012660; Laminin G.
Pfam; PF00008; EGF; 2.
Pfam; PF002210; Laminin G. 2; 2.
                                                                                                       Q4HUZ1 GIBZE E
Q4HUZ1;
13-SEP-2005 (7
13-SEP-2005 (7
13-SEP-2005 (7
                                                                                                                                                                                                                                                                                                           SMART; SM00181; EGF; 2.
SMART; SM00282; LamG; 3.
PROSITE; PS00022; EGF 1;
PROSITE; PS01186; EGF 2;
PROSITE; PS50026; EGF 3;
PROSITE; PS50025; LAM G L
                                        Eukaryota; Fungi; Ascomycota; P. Hypocreomycetidae; Hypocreales; NCBI_TaxID=229533;
                                                                          Hypothetical protein.
ORFNames=FG11217.1;
Gibberella zeae PH-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99069613; PubMed-9851916; The C. elegans semiconi-
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01-WAR-2003 (TrEMBLrel. 23, Last sequence up
01-WAR-2004 (TrEMBLrel. 26, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Intestinal neurexin-like protein 1.
Name=itx-1; ORFNames=W03D8.6;
              STRAIN-PH-1
                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          investigating biology.";
Science 282:2012-2018(1998).
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                      NUCLEOTIDE SEQUENCE
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"Genome sequence of the nematode C. e
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CAEEL
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5 (TrEMBLrel. 31, )
6 (TrEMBLrel. 31,
   Nusbaum C.,
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78.6%;
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   Abouelleil A.,
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Pred. No. 1.5e+02;
1; Mismatches 2;
                                                       Pezizomycotina;
s; Nectriaceae; (
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01-OCT-2000
01-OCT-2003
                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 97:4092-4097(2000).
-!- SIMILARITY: Belongs to the ATPase alpha/beta
EMBL; AF209109; AAF64667.1; -; Genomic_DNA.
HSSP; P19483; 1H8E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Fusarium graminearum genome sequence.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry w
     888888888
                                                                                                                                                                                                                                                                                                                                                                              are conifers."
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Bowe L.M., Coaf G., dePamphills C.W.;
"Phylogeny of seed plants based on all three
extant gymnosperms are monophyletic and Gneta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; & Spermatophyta; Gnetophyta; Spermatophyta; Gnetophyta; Spermatophyta; Spermatophyta; Spermatophyta; Gni TaxID=3383;
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Q9MM39;
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GO:0005739; C:mitochondrion; IEA.
GO:0005739; C:mitochondrion; IEA.
GO:0005261; C:proton-transporting ATP synthase complex; GO:0016469; C:proton-transporting two-sector ATPase complex; GO:0005524; F:ATP binding; IEA.
GO:0005524; F:hydrogen-transporting ATP synthase activity.
GO:0046933; F:hydrogen-transporting ATPase activity, rota.
GO:0046961; F:hydrogen-transporting ATPase activity, TEA.
GO:0016787; F:hydrolase activity; IEA.
GO:0016820; F:hydrolase activity, acting on acid anhydrid.
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L; AACM01000460; E
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368 AA; 4
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63.6%;
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15, Last sequence update)
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(Fragment).
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., Calvo S.E.,
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; Gnetopsida; G
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No. 4:
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Gnetales' clo
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CC :- SMILARITY: Belongs to the ATPase alpha/beta chains family.

DR HSSP; P19483; 1E79.

DR SMR; Q0777A3; 1-418.

DR GO; GO:0005739; C:mitochondrion; IEA.

GO; GO:0005739; C:mitochondrion; IEA.

DR GO; GO:0005739; C:mitochondrion; IEA.

GO; GO:0005524; F:Arp binding; IEA.

DR GO; GO:0016469; C:proton-transporting ATP synthase complex; IEA.

DR GO; GO:0005524; F:Arp binding; IEA.

DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity, rota. .; IEA.

GO; GO:0046933; F:hydrogen-transporting ATP synthase activity, rota. .; IEA.

GO; GO:0046933; F:hydrogen-transporting ATP synthase activity, rota. .; IEA.

DR GO; GO:004693; F:hydrogen-transporting ATP synthase activity, rota. .; IEA.

GO; GO:0016820; F:hydrolase activity; IEA.

DR GO; GO:0016820; F:hydrolase activity, acting on acid anhydrid. .; IEA.

GO; GO:0016820; F:hydrolase activity, acting on acid anhydrid. .; IEA.

GO; GO:0016820; F:hydrolase activity, acting on acid anhydrid. .; IEA.

GO; GO:0016820; F:hydrolase activity, acting on acid anhydrid. .; IEA.

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7A3 GNEGN
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Q1-MAY-2000 (
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Nature 402:404-407(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetophyta; Gnetopsida; Gnetales; Gnetaceae; Gnetum
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9; Conserv
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| |::|||:|| ||:
| TAIIEGSIVKRTGS 59
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Pred. No. 54;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3
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Q6BIS4_DEBHA
ID Q6BIS4_D
AC Q6BIS4;
DT 25-OCT-2
DT 25-OCT-2
DT 25-OCT-2
DT 25-OCT-2
DE Similar
DE function
GN OrderedL
OS Debaryom
OC Eukaryot
OC Saccharo
OX NCBI_Tax
RN (1)
RP NUCLEOTI
RC STRAIN-A
RX PUBMed-1
RA Dujon B.
RA Lafontai
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Best Local S
Matches 9
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Best Local S
Matches 10
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"Cryza sativa nippombare(GA3) genomic I
clone:OSNUBa0039D04.";
Submitted (MAR-2004) to the EMBL/GenBar
Submitted (MAR-2004) to the EMBL/GenBar
EMBL; AP006753; BADD32124.1; -; Genomic_
Gramene; Q691P6; -.
GC; GC:0004194; F:pepsin A activity; II
GO; GC:0004194; F:proteolysis and pepti
                                                                                                                                                                                                                                                                              QGBIS4 DEBHA PRELIMINARY;
QGBIS4;
QGBIS4;
25-OCT-2004 (TrEMBLrel. 28, L
25-OCT-2004 (TrEMBLrel. 28, L
25-OCT-2004 (TrEMBLrel. 28, L
Similar to CA1657 | IPP16022 Ca
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q69IP6;
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00792; PEPSIN.

PROSITE; PS00141; ASP PROTEASE; UNKNOWN
SEQUENCE 451 AA; 46440 MW; E7F24FED
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q69IP6_ORYSA
                          NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
STRAIN-ATCC 36239 / CBS 767;
PubMed=1529592; DOI=10.1038/nature02579;
Dujon B., Sherman D., Fischer G., Durrens P.,
                                                                                                                                                                OrderedLocusNames=DEHA06086799;
Debaryomyces hansenii (Yeast) (Torulaspora hansenii)
Debaryomyces hansenii (Saccharomycotina; Sacc.
Bukaryota; Fungi; Ascomycota; Saccharomycotopes.
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=39947;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00026; Asp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001461; Peptidase_A1.
InterPro; IPR001969; Pept_Asp_AS.
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    Lafontaine
                                                                                                                                          NCBI_TaxID=4959
                                                                                                                                                                                                                                                             function.
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9; Conserve
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DSPILFGSLAKVTGGN
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418 AA;
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    de Montigny J.,
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, Last annotation updat
Candida albicans IPF16
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-; Genomic_DNA.
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Pred. No. !
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Pred. No. 60;
2; Mismatches
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genomic
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       s P., Casaregola
Neuveglise C.,
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                                                                                                                                                                                             Saccharomycetes;
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                             To the human gastrointestinal tract.";

Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).

REMBL; AE014255; AAN25329.1; -; Genomic_DNA.

R HSSP; P25715; IMLA.

R GO; GO:0005835; C:fatty acid synthase complex; IEA.

R GO; GO:0004312; F:fatty-acid synthase activity; IEA.

R GO; GO:0016491; F:oxidoreductase activity; IEA.

R GO; GO:0016740; F:transferase activity; IEA.

R GO; GO:0006131; P:electron transport; IEA.

R GO; GO:0006131; P:electron transport; IEA.

R GO; GO:0006633; P:fatty acid biosynthesis; IEA.

R GO; GO:0006633; P:fatty acid biosynthesis; IEA.

R GO; GO:0006136; P:metabolism; IEA.

R InterPro; IPR00127; Ac transferase.

R InterPro; IPR00127; Ac transferase.

R InterPro; IPR00127; Ac transferase.

R InterPro; IPR003965; Fatty_acid_synth.

InterPro; IPR003965; Fatty_acid_synth.

R InterPro; IPR002539; MaoC_dehydratas.

R Pfam; PF00698; Acyl_transf_1; 1.

R Pfam; PF00109; Ketoacyl-synt; 1.

R Pfam; PF02801; Ketoacyl-synt; 1.

R Pfam; PF02801; Ketoacyl-synt; 1.

R Pfam; PF03575; MaoC_dehydratas; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8G456
Q8G456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; CR382139; CAG90360.1; -; Genomic_I
InterPro; IPR001680; WD40.
Pfam; PP00400; WD40; 6.
SMART; SM00320; WD40; 6.
PROSITE; PS50294; WD REPEATS REGION; 1.
Complete protecome; Repeat; WD repeat.
SEQUENCE 1048 AA; 117153 MW; 7BAEB6(
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Bifidobacteriaceae; Bifido
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Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
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BIFLO
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Pred. No. 1.4e+02;
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MEDLINB=2047337; PubMed=10984043; DOI=10.1038/35023079;

MEDLINB=2047337; PubMed=10984043; DOI=10.1038/35023079;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brink K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";

Nature 406:959-964(2000).

EMBL, AE004754; AAO6712.1; -; Genomic_DNA.
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Complete
SEQUENCE
                                                                                                                                                                                                      HSSP; Q7Z4Wi; 1PR9.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR000073; A/b_hydrolase.
InterPro; IPR002198; ADH_short.
InterPro; IPR002194; Adh_short.
InterPro; IPR002347; Adh_short.
InterPro; IPR002347; Adh_short.
InterPro; IPR000339; Epox hydrolase.
InterPro; IPR000379; Ser_estrs.
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01-MAR-2004 (TrEMBLrel. 26, Last an
Probable short-chain dehydrogenase.
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Q9HYS1;
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PROSITE; PRO0606; B_KETOACYL_SYNTHASE; UNKNOWN
                                                                                                      SEQUENCE
                                                                                                                                         PRINTS; PRO0412; EPOXHYDRLASE. PRINTS; PRO0081; GDHRDH. PRINTS; PRO0080; SDRFAMILY.
                                                                                                                                                                               Pfam; PF00561; Abhydrolase 1; 1. Pfam; PF00106; adh_short; 1.
                                                                                                                                                                                                                                                                                                 PIR; B83231; B83231.
HSSP; Q7Z4W1; 1PR9.
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Pseudomonadaceae; Pseudomonas.
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 PDASSMNGKLVVVTGAGG
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                                                                                                     65770 MW; 7EA0D0996D4D0157 CRC64;
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50.0%;
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Pred. No.
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RESULT 15
Q4ZUU5_PSESY
ID Q4ZUU5_PSESY PRELIMINARY;
AC Q4ZUU5;
AC Q4ZUU5;
DT 13-SEP-2005 (TrEMBLrel. 31,

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A Feil H., Feil W.S., Lindow S.E.;

Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

R EMBL; CP000075; AAY37077.1; -; Genomic_DNA.

R InterPro; IPR005315; AutoCtransporter.

R InterPro; IPR006315; AutoCtransporter.

R InterPro; IPR004899; Pertactin.

R InterPro; IPR003991; Pertactin.

R InterPro; IPR003991; Pertactin.

R InterPro; IPR003991; Pertactin.

R Pfam; PF03997; AutoCtransporter; 1.

R Pfam; PF03979; AutoCtransporter;

R PFAM; PF03991; AutoCtransporter;

R PFAM; PF0399; AutoCtransporter;

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13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Outer membrane autotransporter barrel precursor.
ORFNames=Psyr_2034;
Pseudomonas syringae pv. syringae B728a.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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STRAIN-B728a;
LOPEr J.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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DOE Joint Genome Institute;
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[1]
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75763 MW; 4C355FC1A478A628 CRC64;
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N-PSDB; AAH74579

Designing synthetic nucleic acid sequences for improved amplification, expression in host cell, by comparing free energy of folding of a starring polynucleotide and a modified polynucleotide having a codon replacement.

Claim 6; Page 66-67;

117pp; English

The present sequence represents a NADPH-dependent aldehyde reductase (C (AR2). The polynucleotide sequence was modified using using the method of the invention. The specification describes a method for designing a CC synthetic polynucleotide. The method comprises providing a starting CC polynucleotide, determining the predicted free energy of folding per base of the polynucleotide, modifying the polynucleotide by replacing a codon comparing the polynucleotide of the replacing a codon comparing the provide a modified polynucleotide, determining comparing this with that of the original polynucleotide. The method is comparing this with that of the original polynucleotide. The method is comparing the protein in a heterologous host. The design and preparation of the synthetic genes are used in application of gene shuffling, directed colution and molecular breeding methods. The method allows expression of comparition and molecular breeding methods. The method allows expression of construction and molecular breeding methods. The method allows expression of construction and molecular breeding methods. The method allows expression of construction and molecular breeding methods. The method allows expression of construction and molecular breeding methods. The method allows expression of construction and molecular breeding methods. The method allows expression of construction and molecular breeding methods. The method allows expression of construction and molecular breeding methods. The method allows expression of construction and molecular breeding methods. The method allows expression of construction and molecular breeding methods. The method allows expression of construction and molecular breeding methods. The method allows expression of construction and molecular breeding methods. The method allows expression of construction and molecular breeding methods. The method allows expression of construction and molecular breeding methods. The method allows expression of construction and molecular breeding methods.

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RESULT 5
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DT 15-C
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    Designing
                                                                                         WPI; 2001-483235/52
N-PSDB; AAH74580.
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08-DEC-2000;
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        synthetic nucleic acid sequences for improved amplification
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2000US-00734237
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                                                                                                                                                                                                                 Bui P,
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Disclosure; SEQ ID NO 3; 10pp; English

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RESULT 6
ADO5619
ID ADO55
XX XX ADO55
XX XX ADO55
XX XX Spor
DT 12-A
XX (R)
DT 10-C
XX (MC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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Best Local
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                                                                                                                                                                                                                                                                                                          (MOOR/) MOORE J C.
(STUR/) STURR M G.
(MCLA/) MCLAUGHLIN K.
(KIMJ/) KIM J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 67-68; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression in host cell, by comparing free energy of folding of a starting polynucleotide and a modified polynucleotide having a codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 343 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUL-2003; 2003US-00616320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2004101937-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sporidiobolus salmonicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aldehyde reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sporobolomyces salmonicolor ketoreductase, aldehyde reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-AUG-2004
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                                                                                      comprising
                                                                                                                      Preparing
                                                                                                                                                                                WPI; 2004-431257/40
                                                                                                                                                                                                                                             Moore JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JUL-2002; 2002US-0394761P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (R)-hydroxy ester; alpha-keto ester; ketoreductase; enzyme
aldehyde reductase II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
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                                                                                         (R)-hydroxy ester involves adding alpha-keto ester to mixture
ketoreductase enzyme and non-ketoreductase enzyme components
                                                                                                                                                                                                                                             Sturr MG,
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88.9%;
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4 DNAVL-EGSLVKVTGANG

20 0

Matches Query Match Best Local (

16; Conservative

66.8%;

Score 65.5; DB 4; Pred. No. 0.025; 0; Mismatches 1;

Length 343; Indels 1;

Gaps

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Sequence 343 AA;

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cc sequence of a Bifidobacterium genome selected from the nucleotide CC sequences given in ABQ81842 and ABQ81843, or a sequence given in CC least 90% identity or which hybridises with the sequence given in CC ABQ81842 and ABQ81843. Also described is a polynucleotide (II) encoding a CC fusion protein, comprising a sequence selected from 1097 sequences given in CC in ABP65258 to ABP66354 ligated in frame to a polynucleotide encoding a CC heterologous polypeptide. (I) has antidiarrheic and antibacterial CC aprobe) is useful for the detection and/or identification of CC aprobe) is useful for the detection and/or identification of CC used for preventing and/or treating diarrhoea brought about by pathogenic bacteria and/or rotavirus. The carrier is a food composition selected from milk, yogurt, curd, cheese, fermented milks, milk based fermented corpowders, infant formula, pet food or a pharmaceutical composition cc selected from tablets, liquid bacterial suspensions, dried oral composition of the Bifidobacterium gene. ABQ81844 to ABQ81850 represent CC lis useful in DNA arrays or chips to carry out analysis of the Bifidobacterium related nucleotide sequences given in the Sequence
          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antidiarrheic; antibacterial; inhibitor of Salmonella; detection; identification; lactic acid bacterium; diarrhoea; pathogenic bacteria; rotavirus; food composition; pharmaceutical composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method of preparing high yields of an (R)-hydroxy ester by reducing an alpha-keto ester using a ketoreductase enzyme. The present sequence represents Sporobolomyces salmonicolor ketoreductase, aldehyde reductase II used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                  a probe or primer ior o
in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotide comprising be or primer for detecting
                                                                                                                                                                                                                                                                                                                                                                                                    3; SEQ ID NO 931; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
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Pred. No. 0.02
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bifidobacterium genome sequence useful and/or identifying Bifidobacterium long
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RESULT 9
AAR96967

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RRSULT 8
AAR45942
IID AAR45942
XX AAR45942
XX AAR45
AC AAR4
XX AAR4
XX PFU
DT 22-J
XX Liga
XX Hype
XX Pyro
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                                                                                                                                                      A thermostable DNA ligase from a hyperthermophilic archaebacterium, e.g. p. furiosus, catalyses template-dependent ligation at temps. of 30-80 degrees C, and retains its catalytic ability when subjected to temps. of 85-100 degrees C. The ligase functions effectively in the ligase chain reaction without significant blunt-end ligation. (Updated on 25-MAR-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Listing from the present invention but not mentioned further within the specification. N.B. The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied by the European Patent Office
                                                                                                                                                                                                                                                                    Thermostable DNA ligase from Pyrococcus furiosus - has improved ligation specificity and stability at high temperatures, giving greater efficiency in ligase chain reaction.
                                                                                                             Sequence 561 AA;
                                                                                                                                                                                                                                          Claim 3; Page 62-3; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                         Mathur EJ, Marsh EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9402615-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrococcus furiosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ligase chain reaction; LCR; Pyrococcus furiosus; ligation hyperthermophilic archaebacterium; catalysis; blunt-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfu thermostable DNA ligase
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22-JUL-1994
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 290 IPEKAIVEGELVAI-GENG 307
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10; Conserv
                                                                     Similarity
                            IPDNAVLEGSLVKVTGANG 20
                                                                                                                                           PN field.)
                                                        Conservative
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(first entry)
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                                                                    49.5%;
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Pred. No. 1.5e
4; Mismatches
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                                                                     Score 48.5;
Pred. No. 34;
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                                                         Mismatches
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                                                        Gaps
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RESULT 10
ABU37839
ID ABU37
XX ABU37
XX I9-JU
DT 19-JU
DT Prote
XX Antis
XX Antis
XX Neiss
PN WC200
XX O3-OC
XX O3-OC
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                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                        an esti
field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrococcus furiosus.
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26-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid contg. gene for thermostable DNA ligase – useful in ligase chain reactions, stable up to 100\ \mbox{deg.} C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schoettlin WE, Mathur
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            21-MAR-2002; 2002WO-US009107
                                                                                                        Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                               Protein encoded by Prokaryotic essential gene #23366
                                                                                                                                                          19-JUN-2003
                                                                                                                                                                                                       ABU37839 standard; protein; 636 AA
                                                                                                                                                                                                                                                                                                                                                                 Sequence 561 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Col 29-32; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-200280/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (STRA-)
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                                                            WO200277183-A2
                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                   290
                                                                                                                                                                                                                                                                                                                 l Similarity 52.6
10; Conservative
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|PEKAIVEGELVAI-GENG 307
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52.6%;
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Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                           ВB
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RESULT 11 ADX95802

ADX95802 standard; protein; 947

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268

PDNRLMSADIEGKTVMVTGAGG 289 PDN----AVLEGSLVKVTGANG 20 Query Match
Best Local Similarity
Matches 12; Conserv

Conservative

49.0%;

Score 48; Pred. No.

Length 636; Indels

Mismatches DB 49; 9

4.

Gaps

1;

SEXEXEX

21-APR-2005

(first entry)

Plant full length insert polypeptide seqid 58466

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cc the gene product or that has an activity against a biological pathway contentifying a gene required for cellular proliferation; (8) contentifying a gene required for cellular proliferation or the biological contentifying a gene required for cellular proliferation or the biological contentifying a gene required for cellular proliferation or the biological contentifying a gene on which the test compound that inhibits gene product lies or a gene on which the test compound that inhibits proliferation of an conganism acts; (9) manufacturing an antibiotic; (10) profiling a ccitivity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the gene ccit owhich each of the strains is present in a culture or collection of contentifying the target of a compound that inhibits the croliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required corrections or screening for homologous nucleic acids required corrections or screening homologous nucleic acids covery programs, or for screening homologous nucleic acids covery nucleic acids covery programs, or for screening homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the content of th
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Wall D,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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N-PSDB; ACA41709.
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of the nucleic acid inhibits proliferation of a cell. Also included
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25; SEQ ID NO 65763; 1766pp; English
Sequence
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                                                                           ftp.wipo.int/pub/published_pct_sequences
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Carr GJ,
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Forsyth
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Xu HH;
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CC polynucleotide consisting of a sequence encoding an amino acid sequence CC available in electronic form from the US patent office at CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as CC plant breeding markers. The recombinant DNA construct is useful for CC improving plant tolerance to cold, heat, drought, herbicides, extreme CC osmotic conditions, pathogens or pests, for manipulating growth rate in CC plant cells by modification of the cell cycle pathway, for conferring CC increased resistance to plant disease, for producing galactomannan, CC lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake CC or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of invention.
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ADY22708
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
 ADY22708
                                                                                                                                                                                                                                        Sequence 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 58466; 15pp; English.
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05-NOV-2001;
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                              ADY22708 standard; protein; 965
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(TABA/)
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SCREEN S E.
TABASKA J E.
CAO Y.
                                                                                                                                                                                            Similarity
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                                                                                                              PPNALLSASLLKVAQQNG
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2001US-00985678.
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                                                                                                                                                                                           Score 48; DB
Pred. No. 78;
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PPNALLSASLLKVAQQNG PDNAVLEGSLVKVTGANG Conservative

291 20 <u>۷</u>

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The invention describes a recombinant DNA construct comprising a conjunct polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at confirmation are also useful in physical arrays of molecules and as collective invention are also useful in physical arrays of molecules and as collective improving plant tolerance to cold, heat, drought, herbicides, extreme commotic conditions, pathogens or pests, for manipulating growth rate in collections, pathogens or pests, for particularing growth rate in collection of the cell cycle pathway, for conferring complant cells by modification of the cell cycle pathway, for conferring complant cells by modification. The plant disease, for producing galactomannan, concreased resistance to plant disease, for producing galactomannan, complant growth regulators, for increasing the rate of homologous crecombination in plants, for improving yield by modification of corresponding improved plant growth and development under at least one content. This is the amino acid sequence of a plant full length insert conjugation in the recombinant DNA construct of the
               Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 70492; 15pp; English
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05-NOV-2001;
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               Similarity
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             49.0%;
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Score 48; DB
Pred. No. 80;
2; Mismatches
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PPT 18-FE
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DR N-PSI
DR N-PS
                                                                                                                                                                                                  RESULT 14
ABU39869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cc polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a cc bacterial infection, for evaluating a compound, such as a polypeptide, cc for the ability to bind a P. aeruginosa nucleic acid, as components of cc including anti-P. aeruginosa drugs, as targets for antibacterial drugs, cc including anti-P. aeruginosa drugs, as templates for recombinant cc production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused cc infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequence ABO67826-cc ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed cc sequence data for this patent did not form part of the printed cc sequence appropriates obtained in electronic format from USPTO at xx
   BXAXAXI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 802 AA;
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27-JUL-1998;
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Protein encoded by Prokaryotic essential gene #25396.
                                                         19-JUN-2003
                                                                                                                   ABU39869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENO-) GENOME
                                                                                                                                                                       ABU39869 standard; protein; 6310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to Pseudomonas aeruginosa polypeptides and the
                                                                                                                                                                                                                                                                                                                        464
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98US-0094190P.
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Pred. No.
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CC (1) a vector comprising a promoter operably linked to the interest call (2) a host cell containing the vector; (3) an isolated CC mucleic acid; (4) a host cell containing the vector; (3) an isolated CC polypeptide or its fragment whose expression is inhibited by the CC antisense nucleic acid; (4) an antibody capable of specifically binding CC antisense nucleic acid; (4) an antibody capable of specifically binding CC proliferation or the activity of a gene in an operon required for CC proliferation; (7) identifying a compound that influences the activity of identifying a compound that influences the activity of identifying a gene product or that has an activity against a biological pathway CC required for proliferation, or that inhibits cellular proliferation; (8) CC identifying a gene required for cellular proliferation or the biological compound which the test compound that inhibits proliferation of an CC compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent CC proliferation of the strains is present in a culture or collection of CC strains; or (13) identifying the target of a compound that inhibits the cc proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational CC drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, CC controlled for proliferation of the printed specification, but was obtained con electronic format directly from WIPO at
                                                        Matches
                                                                                 Query Match
Best Local
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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
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Wall
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid

(1) a vector comprising a promoter operably linked to the nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID NO 67793; 1766pp; English.
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AIPDNAVL-----EGSLVKVTGANG 20
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; 2001US-00948993.
; 2001US-0342923P.
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                                                           Conservative
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                                                        Score 47; DB Pred. No. 1.1e 2; Mismatches
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                                                                                                 1.1e+03;
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Forsyth
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Xu HH;
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RESULT 15
ABG28376
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                                                                                                                                                                                                             reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies are states involving (III). (II) is cuseful for generating antibodies are states involving (III). (II) is cuseful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abservant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations or cepsonable for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in fraction in the printed specification of the sequence data for this patent did not appear in the printed specification.
                                                                          Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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N-PSDB; AAS92563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                         Sequence 133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID NO 58735; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                               Similarity
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ACPSKATIPGKTVIVTGAN 23
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Search completed: March 11, 2006, 05:02:22

Job time : 117.921 secs

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PCT-US93-06939-1
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US-08-916-232-1
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                 Sequence 1, Applicati
GENERAL INFORMATION:
APPLICANT: Eric J
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Best Local (
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
                                                                                                                                              APPLICANT: Edward J. Marsh
APPLICANT: Warren E. Schoettlin
TITLE OF INVENTION: Purified Thermostable
TITLE OF INVENTION: Pyrococcus Furiosus DNA
TITLE OF INVENTION: Ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
LIBRARY: Pyroc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 81
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION NUMBER:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM
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CITY: Menlo Park
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pyrococcus Furiosus INDIVIDUAL ISOLATE: DSM #3638 CELL TYPE: unicellular organism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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ilarity 52.6%;
Conservative
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Furiosus DNA Ligase
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Pred. No. 7.
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17830
LENGTH: 802
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LIBRARY: Pyroc
CLONE: pEM1
PCT-US93-06939-1
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                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 278356
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17830, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                     Matches
                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE:
                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/919, FILING DATE: July 23, 1992
ATTORNEY/AGENT INFORMATION NAME: Albert p. Halluin REGISTRATION NUMBER: 25,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 19930722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: STRG 20081 USA TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 433-4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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TELBEAX: 278356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pyrococcus Furiosus
INDIVIDUAL ISOLATE: DSM #3638
CELL TYPE: unicellular organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.5%;
Local Similarity 52.6%;
es 10; Conservative
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464 PDARSMNGKLVVVTGAGG 481
                                                                     10;
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                                  3 PDNAVLEGSLVKVTGANG 20
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                                                                       Conservative
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                                                                                      48.0%;
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Pred. No. 7.
                                                                                        Score 47;
Pred. No.
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19;
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                                                                                                                                            ; ORGANISM: Homo sapiens
US-10-012-231A-116
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Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                             Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 477
SEQ ID NO 116
LENGTH: 331
TYPE: PRT
                                                                    Query Match 46.9
Best Local Similarity 52.6
Matches 10; Conservative
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SEQ ID NO 16593
LENGTH: 308
TYPE: PRT
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                                                                                                                                                                                                                                                                                  APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2830P1C23
CURRENT APPLICATION NUMBER: US/10/012,231A
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APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2002-06-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLICANT:
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Gao, Wei-Qiang
Goddard, Audrey
Goddwski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth J.
ACPSKATIPGKTVIVTGAN 47
                                  AIPDNAVLEGSLVKVTGAN 19
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                                                                                       46.9%;
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Pred. No. 9.4;
5; Mismatches
                                                                      1; Mismatches
                                                                                       Score 46; DB
Pred. No. 10;
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; ORGANISM: Homo sapiens
US-10-006-768A-116
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CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NO 116
LENGTH: 331
LENGTH: 331
                                              Prior Application removed - SEQ ID NO 116 LENGTH: 331
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GENERAL INFORMATION:
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, Davi
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 116, Application US/10006768A Patent No. 6936697
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APPLICANT:
APPLICANT:
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APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C48
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                                                                                             FILE REFERENCE: P2830P1C10
CURRENT APPLICATION NUMBER: US/10/006,768A
CURRENT FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 477
                                                                                                                                                            APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
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                               TYPE: PRT
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Local Similarity 52.6%;
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Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J
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Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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                                                                                                                                                                                                                                                                                                                                                                  Eaton, Dan 1.
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Hillan, Kenneth J.
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                                                                              See File Wrapper or Palm
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Pred. No.
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                                                                                                                                                                                 Polypeptides and Nucleic
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C;Species: Escherichia coli (Strain O157:H7; 8)
C;Date: 16-Feb-2001 #Bequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: D85608; E85659
R;Perna, N.T.; Plunkett III, G; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-778 <KUR>
                                                                                                                                                                                     ISU ribosomal protein L6AB (rp16AB) [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 C;Accession: D90218 C;Accession: D90218 R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Joeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redd arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Vand der Oost, J. submitted to GenBank, April 2001 R;Description: Sulfolopus solfataricus complete genome.
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A;Experimental source: strain O157:H7, substrain EDL933
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A; Residues: 1-111 <ST2>
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A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Genome sequence of enterohemorrhagic Escherichia A;Reference number: A85480; MUID:21074935; PMID:11206551
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A; Accession: D90218
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                                                                A;Cross-references:
                                                                                 A; Molecule type: DNA
A; Residues: 1-181 < KUR>
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                                                                                                                         A, Status: preliminary
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;Gene: AGR_C_1799
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                      Gene:
                                       Genetics:
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Local Similarity 35.0%;
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                                                                  UNIPROT: Q9UX91; UNIPARC: UPI000013416E;
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protein L6/L9
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Pred. No.
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Pred. No. 17;
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                                                                  GB:AE006641; NID:g13813871;
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RESULT 11
A32687
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A;Title: The complete genome of the hyperthermophilic bacterium A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: H70326
                                                                               A,Molecule type: protein
A,Residues: 206-473 cTSU's
A,Cross-references: UNIPARC:UPI000011061E
C;Comment: This protein specifically hydrolyzes lysyl peptide bonds including the Lys-Pr
C;Keywords: hydrolase; serine proteinase
F;1-20/Domain: signal sequence #status predicted <SIG's
F;205-205/Domain: propeptide #status predicted cPRO's
F;206-473/Product: achromobacter proteinase I #status experimental
F;211-421,217-285,241-263/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                       R.Tsunasawa, S.; Masaki, T.; Hirose, M.; Soejima, M.; Sakiyama
J. Biol. Chem. 264, 3832-3839, 1989
A;Title: The primary structure and structural characteristics
A;Reference number: A12960; MUID:89139439; PMID:2492988
A;Accession: A32960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: A32687; A32960
R;Ohara, T.; Makino, K.; Shinagawa, H.; Nakata, A.; Norioka, S.; Sakiyama, J. Biol. Chem. 264, 20625-20631, 1989
A;Title: Cloning, nucleotide sequence, and expression of Achromobacter pro A;Reference number: A32687; MUID:90062204; PMID:2684982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown; tra
A;Molecule type: DNA
A;Residues: 1-371 <AQF>
A;Cross-references: UNIPROT:066644; UNIPARC:UPI00000562FF;
A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein ag 294 - Aquifex aeolicus
C;Species: Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                A.Cross-references: UNIPROT:P15636; UNIPARC:UPI0000125C8B; GB:J05128; NID:g141803; R;Tsunasawa, S.; Masaki, T.; Hirose, M.; Soejima, M.; Sakiyama, F.
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-653 < OHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A32687; A; Accession: A32687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lysyl endopeptidase (EC 3.4.21.50) precursor -
N;Alternate names: Achromobacter proteinase I
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;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004;Accession: H70326
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Pred. No.
Pred. No.
                         Score 46.5;
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Conservative

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Indels

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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-254 <KUR>
A; Residues: 1-254 <KUR>
A; Cross-references: UNIPROT: Q92V10; UNIPARC: UPI00000CB6D2; GB: AL591985; PIDN: CAC49324.1;
A; Experimental source: strain 1021, megaplasmid pSymB
A; Experimental source: strain 1021, megaplasmid pSymB
A; Experimental source: strain 1021, megaplasmid pSymB
A; Galibert, F; Finan, T.M.; Long, S.R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Proc. Natl. Acad. Sci. U.S.A. 98, 9899-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: D95957
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C;Date: 30-Apr-1999 #sequence:
C;Accession: T06029
R;Bevan, M.; Van Der Schueren,
submitted to the Protein Seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable 2-deoxy-D-gluconate 3-dehydrogenase (EC 1.1.1.125) [imported] - Sinorhizobium C;Species: Sinorhizobium meliloti C;Daete: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 05-Oct-2004 C;Accession: D95957
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A;Realdues: 1-532 <BEV>
A;Crose-references: UNIPROT:Q9T069; UNIPARC:UPI00000ABF4D;
A;Experimental source: cultivar Columbia; BAC clone T28I19
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;Species: Arabidopsis thaliana (mouse-ear cress)
;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                      Genome: plasmid
Superfamily: short-chain
                                                                                                                                                                                                                                                Gene: SMb21348
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                                            MAIPDNAVLEGSLVKVTGAN
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ilarity 52.9%;
Conservative
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Sequence Database, March 1999
                                                                                                            43.7%;
                                                                                                                                                                                                    dehydrogenase;
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                                                                                       Score 45; DB
Pred. No. 15;
2; Mismatches
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RESULT 14

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conserved hypothetical protein AF1322 - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004 C;Accession: A69415
C;Accession: A69415
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, F.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kil Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Nature 390, 364-370, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable alcohol dehydrogenase (EC 1.1.1.1) [similarity] - C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_ch C;Accession: T33939 R;Becker, M.; Graves, T.; Wilson, C.
                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-501 < KLE> A;Cross-references: UNIPROT:028947; UNIPARC:UPI0000056D84; GB:AE001012; GB:AE000782;
                                                                                                                                                                                                                                                                                                                                       Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archa
A;Reference number: A69250, MUID:98049343; PMID:9389475
A;Accession: A69415
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A69415
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Search completed: March 11, Job time: 19.3333 secs
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A; Introns: 294/3; 359/3;
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A; Residues: 1-408 <BEC>
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Best Local
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; D. Nackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness,
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Pred. No.
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Pred. No.
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irkness, E.F.,
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RESULT 13
US-10-015-393A-116
; Sequence 116, Application US/10015393A
; Patent No. 6951737
; Patent No. 6951737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 116
LENGTH: 311
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: PERSOPELGY CURRENT APPLICATION NUMBER: US/10/015,671A CURRENT FILING DATE: 2001-12-11
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                            APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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APPLICATION NUMBER: US/10/015,393A
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Desnoyers, Luc
Eaton, Dan 1.
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Desnoyers, Luc
Eaton, Dan 1.
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Gao, Wei-Qiang
Goddard, Audrey
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Godowski, Paul J.
Grimaldi, Christopher J.
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                                                                                   Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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                                                                         Pan, James
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52.6%; Pred. No.
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Pred. No. 10;
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Sequence 116, Application US/10006041A Patent No. 6951921 GENERAL INFORMATION:

APPLICANT:
APPLICANT:

Botstein, David Desnoyers, Luc Eaton, Dan 1.

Ferrara, Napoleone

APPLICANT: APPLICANT: APPLICANT:

Fong, Sherman Gao, Wei-Qiang Goddard, Audrey

Godowski, Paul J

APPLICANT: Baker, APPLICANT: Botste

Kevin P.

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US-10-015-393A-116
RESULT 15
US-10-006-041A-116
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NUMBER OF SEQ ID NOS: 477
SEQ ID NO 116
LENGTH: 331
TYPE: PRT
                                                                                                                                                                               FILE REFERENCE: P2830F1C22

CURRENT FILING DATE: 2002-06-25

Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 477

SEQ ID NO 116

LENGTH: 331

TYPE: PRT

ORGANISM: Homo sapiens
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Patent No. 69519
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Best Local Similarity
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Best Local Similarity 52.6%;
                                                                                                              Matches
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Baker, Kevin P. APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                              APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                    1 AIPDNAVLEGSLVKVTGAN 19
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Gao, Wei-Qiang
Goddard, Audrey
Goddowski, Paul J.
Grimaldi, Christopher J.
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                                                         ACPSKATIPGKTVIVTGAN 47
                                                                                                                                                                                                                                                                                                                                                                   Gurney, Austin L.
Hillan, Kenneth J.
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                                                                                                                Score 46; DB
Pred. No. 10;
1; Mismatches
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Pred. No.
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RESULT 8
US-11-096-568A-20894
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, NAME/KEY: misc_feature

; LOCATION: (1). (388)

; OTHER INFORMATION: Ceres Seq. ID no. 13592517

US-11-096-568A-32256
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US-11-096-568A-20893
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 32256
LENGTH: 388
TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 20894
LENGTH: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20894, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION: APPLICANT: Alexandrov, Nickolai et al.
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 20893
LENGTH: 277
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GENERAL INFORMATION:
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NAME/KEY: misc feature
LOCATION: (1)...(210)
OTHER INFORMATION: Ceres Seq.
1-11-096-568A-20894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Zea mays subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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57.1%;
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Pred. No. 29
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Pred. No.
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Sequence 1267, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA F
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592FUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1). (277)
; OTHER INFORMATION: Ceres Seq. US-11-096-568A-20893
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US-11-096-568A-1267
                                                           ; FEATURE:
NAME/KEY: misc_feature
; LOCATION: (1)..(283)
; OTHER INFORMATION: Ceres Seq.
US-11-096-568A-1266
                                                                                                                                                                                                                                                                                                                                                         US-11-096-568A-1266
                                                                                                                                                                               TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT ELING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 1266
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SEQ ID NO 1267
LENGTH: 246
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Best Local
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Best Local Similarity Matches 11; Conserv
                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Zea mays subsp.
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                                                                                                                                       TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                                                                       LENGTH: 283
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milarity 57.1%;
Conservative
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                 40.3%;
57.9%;
   Score 41.5; D
Pred. No. 29;
1; Mismatches
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Pred. No. 24
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                                 Length 283;
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Conservative

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NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 1265

LENGTH: 316

TYPE: PRT

ORGANISM: Zea mays subsp. mays
PEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(316)
OTHER INFORMATION: Ceres Seq. ID no. 13
US-11-087-099-4990
; Sequence 4990, Application US/11087099
; Publication No. US20060041961A1
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US-11-096-568A-1265
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APPLICANT: Alexandrov, Nickolai et al.
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION UNMEER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
                                                                                                                                                                                                                                                                                                              SEQ ID NO 211
LENGTH: 1562
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Best Local
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                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC
                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Streptococcus mutans UA159
                                                                                                                                                                           Local Similarity 52.6%; tes 10; Conservation
                                                                                                             1210 PEEALELRQDLVKITDANG 1228
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; FEATURE:
, NAME/KEY: misc feature
; LOCATION: (1)..(234)
; OTHER INFORMATION: Ceres Seq. ID no. 14313384
US-11-096-568A-12932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Watches 8; Conserve
Search completed: March 11, 2006, 05:16:53 Job time : 12.3333 secs
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US-11-087-099-4990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-096-568A-12932
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1293, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(5)450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 4990
LENGTH: 175
                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 12932
LENGTH: 234
TYPE: PRT
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                                                                                                                                 Matches
                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                  ORGANISM: Triticum aestivum
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                                                                                                                                               Local
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8; Conserv
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                                                                 PDGFCIESNVVKVLGA 86
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Pred. No.
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27;
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APPLICANT:

Bui, Peter

SYNTHETIC GENES FOR ENHANCED EXPRESSION

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TITLE OF INVENTION: SYNTHETIC GENES FOR ENHAN
FILE REFERENCE: B583:53896
CURRENT APPLICATION NUMBER: US/10/989,488A
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: 09/494,921
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 09/734,237
PRIOR APPLICATION NUMBER: 09/734,237
PRIOR APPLICATION NUMBER: 09/734,237
PRIOR APPLICATION NUMBER: 09/734,237
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 3.5
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                                                                                                                                       US-10-437-963-171580
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                                                                        Sequence 171580, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hua, Ling
TITLE OF INVENTION: SYNTHETIC GENES FOR ENHANCED EXPRESSION
FILE REFERENCE: B583:53896
CURRENT APPLICATION NUMBER: US/10/989,488A
CURRENT FILING DATE: 2004-11-15
PRIOD ADDOT TOWNSTON.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/734,237
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rozzell, J. David
APPLICANT: Bui, Peter
APPLICANT: Hua, Ling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/494,921
PRIOR FILING DATE: 2000-01-31
                                         APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Sporidiobolus salmonicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 343
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                l Similarity
18; Conserv
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Kovalic, Davi
Zhou, Yihua
Cao, Yongwei
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                                       David K
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
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                                                                                  PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 17180
LENGTH: 279
TYPE: DET
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publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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SEQ ID NO 65763
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APPLICANT:
APPLICANT:
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                                          Remaining Prior Application data NUMBER OF SEQ ID NOS: 78614
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: ELITRA.034A
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ORGANISM: Oryza sativa
                        SOFTWARE: PatentIn version 3.1
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10; Conserv
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Yamamoto, Robert
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nilarity 62.5%;
Conservative 2
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Pred. No. 6.
                                                                       removed
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6.9;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 273937
LENGTH: 892
; FEATURE:
; OTHER INFORMATION: Clone ID: 700383178_FLI.pep
US-10-425-114-58466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_181416C.1.pep
US-10-425-115-273937
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US-10-425-114-58466
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Best Local Similarity 54.5%;
Matches 12; Conservative
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Best Local (
                                                                                                                             SEQ ID NO 58466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                               APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TILE REFERENCE: 38-21(53313)B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
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                                                         ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: unsure
LOCATION: (1)..(892)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                            LENGTH: 947
TYPE: PRT
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Similarity 55.6%;
10; Conservative
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    Mismatches

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Pred. No. 58;
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Pred. No.
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APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 70492

LENGTH: 965

TYPE: DET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73025E08_FLI.pep
US-10-425-114-70492
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US-10-425-114-70492
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 67793, Application US/10282122A
Publication No. US20040029129A1
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Best Local Similarity
Matches 10; Conser
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                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
          TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITAA.034A
CURRENT APPLICATION UNMESER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Liangeu
APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -10-282-122A-67793
                                                                                                                                                                                                         APPLICANT:
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 FILING DATE:
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                                                                                                                                                                                                                                                                                                         Ohlsen, Kari
Zyskind, Judith
                                                                                                                                                                                                                                   Carr, Grant
Carr, Robert
                                                                                                                                                                                                                     Yamamoto, Ro
Foreyth, R.
                                                                                                                                                                                                                                                                          Trawick, John
                                                                                                                                                                                                                                                                                          Wall, Daniel
                                                                                                                                                                                                                                                                                                                                              Haselbeck, Robert
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2000-09-06
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Pred. No.
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96;
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RESULT 15
US-10-450-763-58735
US-10-450-763-58735
Sequence 58735, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOPTWARE: Patentin version 3.1
SEQ ID NO 67793
SEQ ID NO 67793
FENGTH: 6310
TYPE: PRT
ORGANISM: Pseudomonas putida
US-10-282-122A-67793
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; NAME/KEY: DOMAIN
; NAME/KEY: DOMAIN
; LOCATION: (15)..(131)
COTHER INFORMATION: short chain dehydrogenase domain identified by PFam,
; OTHER INFORMATION: accession name adh_short, E-value=9.1e-05, PFam score of -12.5
US-10-450-763-58735
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PRIOR FILLING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILLING DATE: 2000-10-33
PRIOR PILLING DATE: 2000-11-27
PRIOR PPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILLING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILLING DATE: 2001-02-16
PRIOR FILLING DATE: 2001-02-16
                                                                                         Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 58735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 45.6%;
Best Local Similarity 37.5%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR PELING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/649,167 PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: DOMAIN
LOCATION: (92)..(104)
OTHER INFORMATION: GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE domain
OTHER INFORMATION: identified by eMATRIX, accession number PR00081B, p-value=6.727e-
OTHER INFORMATION: 11, raw score of 10.38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH: 133
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                                      2 AIPDNAVLEGSLVKVTGAN 20
                                                                                           10; Conservative
                                                                                                                  h 44.7%;
Similarity 52.6%;
ACPSKATIPGKTVIVTGAN 23
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Pred. No. 1.3e+03;
2; Mismatches 6
                                                                                      Score 46; DB 5;
Pred. No. 19;
1; Mismatches
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Search completed: March 11, 2006, 05:16:12 Job time : 97.3333 secs

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RESULT 6
PCT-US93-06939-1
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US-08-916-232-1
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                     Sequence 1, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDIVIDUAL ISOLATE: DSM #3638
CELL TYPE: unicellular organism
IMMEDIATE SOURCE:
LIBRARY: PYROCCUP
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 47.1%;
Best Local Similarity 52.6%;
Matches 10; Conservative
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WordPerfect 5.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PU
TITLE OF INVENTION: FU
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 81
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                              NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach &
                                                                                                                                APPLICANT: Edward J. Marsh
APPLICANT: Warren E. Schoettlin
TITLE OF INVENTION: Purified Thermostable
TITLE OF INVENTION: Pyrococcus Furiosus DNA
TITLE OF INVENTION: Ligase
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein ORIGINAL SOURCE:
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
STREET: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Menlo Park
                                                           ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 415-854-3660
                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                             290 IPEKAIVEGELVAI-GENG 307
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2730 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                  USA
                                                                                                                                                                                                                                       Eric J. Mathur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyroccus Furiosus Genomic DNA
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Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 561;
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PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17830
LENGTH: 802
Type: Dam
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                                                                                                                                       ORGANISM: Pseudomonas aeruginosa US-09-252-991A-17830
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17830, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                   Matches
                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                              APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
LIBRARY: Pyroc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: STRG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEPAX: (415) 433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: July 23, 19
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pyrococcus Furiosus INDIVIDUAL ISOLATE: DSM #3638 CELL TYPE: unicellular organism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.1%;
Local Similarity 52.6%;
es 10; Conservative
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Pred. No. 7.7;
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RESULT 9
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US-08-849-602C-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4139
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5
CURRENT APPLICATION NUMBER: US
APPLICATION NUMBER: US
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TITLE OF INVENTION: ACHROMOBACTER PROTEASE I GENE AND GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/849,602C FILING DATE: 02-JUN-1997 CLASSIFICATION: APPRODNEY / APPROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 20-FEB-1990
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STRANDEDNESS: sir
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   VAIPDNATVE-SPITVSGRTG 587
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Pred. No. 20;
4; Mismatches
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US-09-248-796A-16593
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CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 16593
                                                                                                                                                                                          Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 116
LENGTH: 331
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PRETENT NO. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
APPLICANT: NOUTEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAMONSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
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APPLICANT:
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APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C23
                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/012,231A CURRENT FILING DATE: 2002-06-10
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                                                                    . Similarity 10; Conserv
 ACPSKATIPGKTVIVTGAN 47
                                 AIPDNAVLEGSLVKVTGAN 20
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Gao, Wei-Qiang
Goddard, Audrey
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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Botstein, David
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Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 477
SEQ ID NO 116
LENGTH: 331
TYPE: PRT
ORGANISM: Homo Bapiens
US-10-015-389A-116
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US-10-015-389A-116
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Best Local (
                           Prior Application removed -
SEQ ID NO 116
LENGTH: 331
TYPE: PRT
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APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan 1.
APPLICANT: Ferrara, Napole
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Patent No. 693669
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                          APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERENCE: P2830P1C10
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                                                                                             CURRENT APPLICATION NUMBER: US/10/006,768A CURRENT FILING DATE: 2002-03-05 NUMBER OF SEQ ID NOS: 477
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APPLICANT: Botstein, David
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ORGANISM: Homo sapiens
10-006-768A-116
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Gao, Wei-Qiang
Goddard, Audrey
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Hillan, Kenneth J.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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Grimaldi, Christopher J.
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Eaton, Dan 1.
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                                                                                  See File Wrapper or Palm
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US-10-015-671A-116
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US-10-015-393A-116
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Matches 10; Conserv
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NUMBER OF SEQ ID NOS: 477
SEQ ID NO 116
LENGTH: 331
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APPLICANT: Baker, K
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: PERSOPPICAT
CURRENT APPLICATION NUMBER: US/10/015,671A
CURRENT FILING DATE: 2001-12-11
CURRENT FILING DATE: 2001-12-11
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ORGANISM: Homo sapiens
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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Local Similarity 52.6%;
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Godowski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth J.
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Gao, Wei-Qiang
Goddard, Audrey
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Fong, Sherman
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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Desnoyers, Luc
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Eaton, Dan 1.
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CURRENT PAPLICATION NUMBER: US/L/O/D15,393A

CURRENT PAPLICATION AMER 2020-61-00

Prior Application removed - See File Wrapper or Palm

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08-DEC-2000; 2000US-00734237
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       Designing synthetic nucleic acid sequences for improved amplification
                                                                                     N-PSDB; AAH74580
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                                                                 comprising
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(STUR/) STURR M G.
(MCLA/) MCLAUGHLIN K.
(KIMJ/) KIM J.
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                                                              (R)-hydroxy ester involves adding alpha-keto ester to mixture y ketoreductase enzyme and non-ketoreductase enzyme components
                                                                                                                                                                              Sturr MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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81.8%;
                                                                                                                                                                                Mclaughlin K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 68.5; DB 4
Pred. No. 0.0088;
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                                                                                                                                                                                   Kin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Disclosure; SEQ ID NO 3; 10pp; English

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RESULT 7
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CC sequences given in AB081842 and AB081843, or a sequence exhibiting at CC least 90% identity or which hybridises with the sequence spiven in CC AB081842 and AB081843. Also described is a polymucleotide (II) encoding a CC in AB985258 to AB966354 ligated in frame to a polymucleotide encoding a CC detrologous polypeptide. (I) has antidiarrheic and antibacterial CC aprobe) is useful for the detection and/or identification of sequence spiven in a probe) is useful for the detection and/or identification of containing the CC aprobe) is useful for the detection and/or identification of containing the CC aprobe) is useful for the detection and/or identification of containing the CC aprobe) is useful for the detection and/or identification of can be used for preventing and/or treating diarrhoea brought about by pathogenic bacteria and/or rotating the carrier is a food composition selected CC bacteria and/or rotating the carrier is a food composition selected CC products, ice-creams, fermented cereal based products, milk based for products, intent formula, pet food or a pharmaceutical composition containing the selected from tablets, liquid bacterial suspensions, dried oral susplement, dry tube feeding or wet tube feeding. CC supplement, wet oral supplement, dry tube feeding or wet tube feeding. CC Expression of the Bifidobacterium gene. AB081844 to AB081850 represent CC Bifidobacterium related nucleotide sequences given in the Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ś
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bifidobacterium longum NCC2705; Bifidobacterium; bacterial; antidiarrheic; antibacterial; inhibitor of Salmonella; detection; identification; lactic acid bacterium; diarrhoea; pathogenic bacteria; rotavirus; food composition; pharmaceutical composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method of preparing high yields of an (R)-hydroxy ester by reducing an alpha-keto ester using a ketoreductase enzyme. The present sequence represents Sporobolomyces salmonicolor ketoreductase, aldehyde reductase II used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bifidobacterium longum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP66187 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a polynucleotide (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; SEQ ID NO 931; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nove1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001EP-00102050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NEST )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ovel polynucleotide comprising probe or primer for detecting n a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bifidobacterium genome sequence useful and/or identifying Bifidobacterium long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
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RESULT 9
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RESULT 8
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                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                 P. furiosus, catalyses template-dependent ligation at temps. of 30-80 degrees C, and retains its catalytic ability when subjected to temps. of 85-100 degrees C. The ligase functions effectively in the ligase chain reaction without significant blunt-end ligation. (Updated on 25-MAR-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermostable DNA ligase from Pyrococcus furiosus - has improved ligation specificity and stability at high temperatures, giving greater efficiency in ligase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listing from the present invention but not mentioned further with specification. N.B. The sequence data for this patent is not reprint the printed specification but is based on sequence information supplied by the European Patent Office
                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                              A thermostable DNA ligase from a hyperthermophilic archaebacterium, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-048873/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ligase chain reaction; LCR; Pyrococcus furiosus; ligation; hyperthermophilic archaebacterium; catalysis; blunt-end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
22-JUL-1994
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                                                                                                                                                                                                                                                 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 62-3; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ55729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUL-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyrococcus furiosus.
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                                                                                                                        Similarity
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  IPEKAIVEGELVAI-GENG
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Pred. No. 1.7e
4; Mismatches
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Pred. No. 3
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                                                                                                                        38;
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1.7e+02;
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RESULT 10
ABU37839
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of a purified thermostable DNA ligase isolated from a hyperthermophilic marine archaebacterium, Pyrococcus furiosus (Pfu). The Pfu DNA ligase catalyese template dependent ligation at temperatures of about 30-80 deg.C. and substantially retains its catalytic ability when subjected to temperatures of 85-100 deg.C. It has an estimated mol. wt. of 50-70 kba. (Updated on 25-MAR-2003 to correct PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thermostable ligase; Pfu; Pyrococcus furiosus; ligase chain reaction; LCR; template dependent ligation.
                                                                                                                                                                  ABU37839
                                                                                                                                                                                                                                                                                                                                     Sequence 561 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Col 29-32; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid contg. gene for thermostable DNA ligase – useful in ligase chain reactions, stable up to 100 deg. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schoettlin WE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfu DNA ligase
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26-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR96967 standard; protein; 561 AA
                                                                                                                                            19-JUN-2003
                                                                                                                                                                                       ABU37839 standard; protein; 636 AA
         21-MAR-2002; 2002WO-US009107.
                                03-OCT-2002
                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                   Protein encoded by Prokaryotic essential gene #23366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (STRA-) STRATAGENE
                                                     WO200277183-A2
                                                                         Neisseria meningitidis
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DB; AAT14926.
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                                                                                                                                                                                                                                                                                          Conservative
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(first entry)
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52.6%;
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                                                                                                                                                                                                                                                                                         4; Mismatches
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Pred. No. 38;
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RESULT 11
ADX95802
ID ADX95

ADX95802 standard; protein; 947

XXXXXX

21-APR-2005

(first entry)

Plant full length insert polypeptide seqid 58466

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268 4

PDNRLMSADIEGKTVMVTGAGG 289

PDN----AVLEGSLYKYTGANG 21 Conservative

1:

Mismatches

<u>ب</u>

Indels

4

Gaps

1.

Query Match
Best Local Similarity
Matches 12; Conserv

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression confiction of the nucleic acid inhibits prodiferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense conclete acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable (6) inhibiting cellular containing the polypeptide; (6) an isolated containing the polypeptide; (7) an isolated containing the polypeptide; (8) an isolated station; (9) the polypeptide; (8) inhibiting cellular containing the polypeptide; (8) inhibiting cellular proliferation or that that an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation; (8) cidentifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an organism acts provide the compound that inhibits proliferation of an organism; or (11) identifying the target of a compound that inhibits the extent to which each of the strains is present in a culture or collection of containing the carget provide activity in the target of a compound that inhibits the extent contains of the proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, contained in electronic format directly from WIPO at the contained of the strained specification, but was obtained contained in t
                                                                  21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID NO 65763; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-029926/02.
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                                                                                                              ftp.wipo.int/pub/published_pct_sequences
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Carr GJ,
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46.6%;
    Score 48;
Pred. No.
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         DB
54;
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Forsyth
                             Length 636;
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Xu HH;
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RESULT 12
ADY22708
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                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a recombinant DNA construct comprising a collection of a sequence encoding an amino acid sequence available in electronic form from the US patent office at electronic form from the US patent office at collection of the invention are also useful in physical arrays of molecules and as collecting plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme communic conditions, pathogens or pests, for manipulating growth rate in colls by modification of the cell cycle pathway, for conferring conformation in plants, for improving yeal actomannan, compliant cells by modification of the cell cycle pathway, for conferring conformation in plants, for improving yield by modification of composition of plants growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of conformation or plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert content. This is the amino acid sequence of a plant full length insert protein yield and/or prot
                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 10; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plant protectant; plant growth regulant; gene therapy; plant recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactcomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                          Sequence 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 58466; 15pp; English.
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05-NOV-2001;
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  ADY22708
                                          ADY22708 standard; protein; 965
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(/rurl)
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TABASKA J E.
CAO Y.
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2001US-00985678
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Pred.
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PPNALLSASLLKVAQQNG

2; 21 291

Matches

Conservative

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CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide CC of the invention are also useful in physical arrays of molecules and as color plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme common conditions, pathogens or pests, for manipulating growth rate in CC plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, CC ilgnin or plant growth regulators, for increasing the rate of homologous creombination in plants, for improving yield by modification of construct of the photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake CC or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the
Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production, lighin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                 polynucleotide consisting of a sequence encoding an amino available in electronic form from the US patent office at
                                                                                                                                                                                                                                                                                                                                                                       The invention describes a recombinant DNA construct comprising polynucleotide consisting of a sequence encoding an amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 70492; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu
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05-NOV-2001; 2001US-00985678
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SCREEN S E.
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CAO Y.
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Similarity
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                                                    965
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46.6%;
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Score 48;
Pred. No.
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                Length 965;
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ADV65680
ID ADV65680
XX ADV656
XX ADV65
XX ADV65
XX O2-JU
DT O2-JU
DT O2-JU
DX Schig
KW diagr
XX WO200
XX WO200
XX WO200
YX Verj
PR 11-SI
XX II-SI
XX Verj
PF Deman
PF Diams
PF Diams
PF User
XX WPI;
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                          protein, a hybridoma cell line which produces the isolated antibody, a method for determining a S. mansoni infection in a subject and a computer readable medium having recorded in it a nucleic acid molecule from S. mansoni genome. The nucleic acid molecule is useful for preventing, diagnosing, or treating S. mansoni infection (schistosomiasis). It can also be used as vaccine against S. mansoni. The present sequence is a Schistosoma mansoni protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/jublished_pot_sequences. Also, SEQ ID 2141-2152 are mentioned in the specification but are not included in the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid molecule encoding a Schistosoma mansoni protein, useful for as a vaccine or for preventing, diagnosing, or treating Schistosoma mansoni infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schistosoma mansoni.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schistosomacide; schistosomiasis; psychiatric disorder; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S. mansoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid molecule encoding a Schistosoma mansoni protein, or its portion which is at least 20 amino acids in length. Also included are an expression vector comprising the nucleic acid operably linked to a promoter, a recombinant cell transformed/transfected with the nucleic acid (or expression vector), a recombination vector).
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                                                                                                                                                     Sequence 272 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              comprising an amino acid sequence encoded by the nucleic acid, an immunogenic composition comprising the isolated S. mansoni protein, an isolated antibody which specifically binds to the isolated S. mansoni protein, a hybridoma cell line which produces the isolated antibody, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogenic composition comprising the nucleic acid in combination with pharmaceutical adjuvant or carrier, an isolated S. mansoni protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 1098; 52pp; English.
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Demarco R, Garcia JCL,
Dias-Neto E, Setubal JC,
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C, Menck CFM,
                                                                           4.
                                                                                              Score
Pred.
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Madeira
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29;
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, Nascimento ALTO;
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RESULT 14

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to Pseudomonas aeruginosa polypeptides and the CC polynucleotides encoding them. The sequences are useful in diagnostics, therapy of pathological conditions, as molecular targets for diagnostics, CC prophylaxis and treatment of pathological conditions resulting from a conditions resulting from a condition of the ability to bind a P. aeruginosa nucleic acid, as components of CC for the ability to bind a P. aeruginosa nucleic acid, as components of CC including anti-P. aeruginosa drugs, as targets for antibacterial drugs, conduction of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused components for diagnosis and/or treatment of P. aeruginosa-caused components for diagnosis and/or treatment of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed conspection of the patent of the printed conspection of the prin
                                                                                                                                                                                                                                                                                        ABU39869
                                                                                                                                                                                                                                                                                                                      RESULT 15
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Matches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacterial infection; Pseudomonas aeruginosa infection; antibacterial
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27-JUL-1998;
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                              Protein encoded by Prokaryotic essential gene #25396.
                                                                                                      19-JUN-2003
                                                                                                                                                                              ABU39869;
                                                                                                                                                                                                                                              ABU39869 standard; protein; 6310
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98US-0094190P.
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Pred. No. 1e+02;
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Pseudomonas putida.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

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cc the 513 antisense squences given in the specification where expression cc (1) a vector comprising a promoter operably linked to the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid cencoding a polypeptide whose expression is inhibited by the antisense cc nucleic acid; (2) a host cell containing the vector; (3) an isolated copolypeptide or its fragment whose expression is inhibited by the antisense cc proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an occompound that inhibits proliferation of an organism. The antisense nucleic acids are useful for strains; or (11) identifying the target of a compound that inhibits the compound that inhibits reduced to the target prokaryoti
                                                                                                                                                                     Query Match
Best Local &
                                                                                                                                       Matches
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Wall D,
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                   Sequence 6310 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to an isolated nucleic acid comprising any one of
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Trawick JD,
                                                                  AIPDNAVL------EGSLVKVTGANG 21
                                                                                                                                           Conservative
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Carr GJ,
                                                                                                                                                                         45.6%;
37.5%;
                                                                                                                                       2; Mismatches
                                                                                                                                                                            Score 47; DB 6; Length 6310; Pred. No. 1.2e+03;
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Xu HH;
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밁 Ś Search completed: March 11, 2006, 05:02:25 Job time: 120.667 secs

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FILE REFERENCE: B583:53896
CURRENT APPLICATION NUMBER: US/10/989,488A
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: 09/494,921
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 09/734,237
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin version 3.2
SEQ ID NO 35
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; TYPE: PRT
; ORGANISM: Sporidiobolus salmonicolor
US-10-989-488A-35
                                                                        US-10-437-963-171580
Sequence 171580, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
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Publication No.
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PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 09/734,237
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hus, Ling
TITLE OF INVENTION: SYNTHETIC GENES FOR ENHANCED EXPRESSION
FILE REPERENCE: B563:53896
CURRENT APPLICATION NUMBER: US/10/989,488A
CURRENT FILING DATE: 2004-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rozzell, J. David
APPLICANT: Bui, Peter
APPLICANT: Hua, Ling
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                                     APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Synthetic protein derived from Sporidiobolus salmonicolor OTHER INFORMATION: NADPH-Dependent Aldehyde Reductase 2, having an ala to gly OTHER INFORMATION: mutation at amino acid position 2
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 343
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Kovalic, Davi
Zhou, Yihua
Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/10989488A
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milarity 88.9%;
Conservative
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                                                                                                                                                                                                                                                                                          Score 65.5; DB 5; Length 343; Pred. No. 0.031;
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Pred. No. 0.031;
0; Mismatches 1;
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APPLICANT: Boukharov, APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Note and Other Molecules Asso
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 171580
LENGTH: 279
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                                                                                                                                                                                                       PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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APPLICANT:
APPLICANT:
SOFTWARE: PatentIn version 3.1 SEQ ID NO 65763
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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APPLICANT:
APPLICANT:
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                                     Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 78614
                                                                                PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
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ORGANISM: Oryza sativa
FEATURE:
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10; Conserv
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Trawick, John
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Malone, Cheryl
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Yamamoto, Robert
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llarity 62.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 279;
                                                                 See File Wrapper or PALM
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Caco, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION DATE: 2003-04-28
JUMBER OF SEQ ID NOS: 73128
SEQ ID NO 58466
LENGTH: 947
TYPE: PRT
TYPE: PRT
TYPE: PRT
TRANSM: Zea mays
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US-10-425-115-273937
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US-10-425-115-273937
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US-10-425-114-58466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-425-114-58466
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Best Local (
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SEQ ID NO 273937
LENGTH: 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 273937, Application US/10425115 Publication No. US20040214272A1
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-64-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: unsure
LOCATION: (1)..(892)
OTHER INFORMATION: unsure at all Xaa locations
                  OTHER INFORMATION: Clone ID: 700383178_FLI.pep
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Similarity 55.6%;
10; Conservative
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APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313) B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILLING DATE: 2003-04-28

INUMBER OF SEQ ID NOS: 73128

SEQ ID NO 70492

LENGTH: 965

TYPE: ppr
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Best Local S
Matches 10
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Cheryl
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APPLICANT:
APPLICANT:
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        TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
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FILING DATE:
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Carr, Grant
Carr, Robert
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Zyskind, Judith
                                                                                                                                                                                                          Yamamoto, Rorsyth, R.
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2000-09-06
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Pred. No.
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Pred. No.
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Sequence 58735, Application US/10450763
; Sequence 58735, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
ITILE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PC7/US01/08631
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2001-03-31
; PRIOR FILING DATE: 2000-08-23
; PRIOR FILING DATE: 2000-08-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 67793
LENGTH: 6310
TYPE: PRT
ORGANISM: Pseudomonas putida
US-10-282-122A-67793
                                                                                                                                                                                             ; FEATURE:
; NAME/KEY: DOWAIN
; LOCATION: (15)..(131)
; OTHER INFORMATION: short chain dehydrogenase domain identified by PFam,
; OTHER INFORMATION: accession name adh_short, E-value=9.1e-05, PFam score of -12.5
US-10-450-763-58735
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PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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Best Local Similarity 37.5%;
Matches 12; Conservative
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SOFTWARE: Custom
SEQ ID NO 58735
                                                                                             Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (92)...(104)
OTHER INFORMATION: GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE domain
OTHER INFORMATION: identified by eMATRIX, accession number PR00081B, p-value=6.727e-
OTHER INFORMATION: 11, raw score of 10.38
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Pred. No. 1.2e+03;
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Pred. No. 18;
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EMBL; BX649605; CR47862.1; -, Genomic DNA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR001509; Epimerase Dh.
Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley., Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J., Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J., Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S., Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R., Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A., Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A., Boldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B., Haaris D., Horiuchi H., Huang J., Humphrey S., Jimenez J., Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R., Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R., Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C., Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C., Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C., Majoros W.H., May G.S., Miller B.L., Mchamoud Y., Molina M., Monod M. Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I., Paralaya M.A., Pertea M., Price C., Pritchard B.L., Quail M.A., Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
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ORFNames=AfA24A6.070c;
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PubMed=14998527; DOI=10.1016/j.fgb.2003.12.003;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Eukaryota; Fungi; Ascomycota;
Eurotiales; Trichocomaceae; mi
NCBI_TaxID=330879;
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13-SEP-2005 (TrEMBLrel.
Aldehyde reductase II.
ORFNames=Afulg11360;
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Asperg
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RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
RA Choepel Y., Collymore A., Cook S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook P., Cooke P., Corum B., DeArellano K.,
RA Choepel Y., Collymore A., Cook P., Cooke P., Corum B., DeArellano K.,
RA Choepel Y., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Plerre N., Hafez N.,
RA Gardyna S., Gnerre S., Graham L., Grand-Plerre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulne W., Iliev I.,
RA Hagopian D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., McClarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Milsen C.B., Norbu C., O'Connor T., O'Onnnell P., O'Neil D.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Onnnell P., O'Neil D.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Ramas J., Tesfaye S., Thoodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Lander R., Senther B., Stange-Thomann N., Stofjanovic N., Stubbs M.,
RA Lander R., Senther B., Zandeor J., Zembek L., Zimmer A., Zody M.,
RA Lander R., Senther R., Zandeor J., Zembek L., Zimmer A., Zody M.,
RA Lander R., Senther R., Senther R., Zander R., Zody M.,
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Romning C.M., Rutter S., Salzberg S.L., Sanchez M.,
Sanchez-Ferrero J.C., Saunders D., Seger K., Squares R., Squares S.,
Takeuchi M., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman J.,
White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
Wanchida M., Hall N., Barrell B., Denning D.W.;
"Genomic sequence of the pathogenic and allergenic filamentous fungus
"Genomic sequence of the pathogenic and allergenic filamentous fungus
"Bapergillus funigatus.";
L. Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
"C. -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
"C. preliminary data.
"R. EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
"SEQUENCE 352 AA; 39420 MW; 0E84223EEC67ABF9 CRC64;
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Hypothetical
SEQUENCE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus nidulans FGSC A4.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
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Q5ASZ7;
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                                                                                                                                                                                  "Genome Sequence of Aspergillus nidulans.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                     CAUTION: The sequence shown here
                                                                                                                       preliminary data.
                                                                                                                                             EMBL/GenBank/DDBJ whole genome
                                                                                                      AACD01000158; EAA60617.1; -; Genomic_
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13-SEP-2005
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Hypothetical protein.
ORFNames-PFL 0235;
Pseudomonas fluorescens (strain Pf-5).
Pseudomonas fluorescens (strain Pf-5).
                                                                                                                                                     PubMed=15980861; DOI=10.1038/nbt1110;
Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
Mavrodi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
Mavrodi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Rosovitz M.,
Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,
Khouri H.M., Pierson E., Pierson L. III, Thomashow L., Loper J.;
"Complete genome sequence of the plant commensal Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S., Mavrodi D., DeBoy R.T., Seshadti R., Ren Q., Madupu R., Dodson R. Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K. Khouri H.M., Pierson E., Pierson L. III, Thomashow L., Loper J., "Complete genome sequence of the plant commensal Pseudomonas fluorescens Pf-5.";
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
Phenylacetic acid degradation protein PaaN.
Name=paaN; ORFNames=PFL 3140;
Pseudomonas fluorescens (strain Pf-5).
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Pseudomonadaceae; Pseudomonas
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EMBL; CP000076; AAY95646.1; -; Genomic_DNA
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                                                                                                                    "Complete genome sequence fluorescens Pf-5.";
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"Large-Scale Engineering of the Corynebacterium gl'
Appl. Environ. Microbiol. 71:3369-3372(2005).
EMBL; AB19303; BAD84061.1; -; Genomic_DNA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
GO; GO:0008152; P:metabolism; IEA.
GO; GO:0008152; P:metabolism; IEA.
GO; GO:0008152; P:metabolism; IEA.
GO; GO:00181002086; Aldehyd dehydrog.
InterPro; IPR002539; MaoC_dehydratas.
InterPro; IPR011966; PaaN-DH.
Pfam; PF00171; Aldedh; 1.
Pfam; PF01575; MaoC_dehydratas; 1.
TIGRFAM6; TIGR0228; PaaN-DH; 1.
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10-MAY-2005
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                                 NUCLEOTIDE SEQUENCE.

STRAIN-R1 / ATCC 13939 / DSM 20539 / NCIB 9279;

MEDLINE-20036896; pubMed=10567266; DOI=10.1126/science.286.5444.1571;

Mhite O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,

Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,

Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,

Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,

Vanathevan X.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,

Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
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Suzuki N.,
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Putative aldehyde dehydrogenase.

Corynebacterium glutamicum (Brevibacterium flavum).

Bacteria; Actinobacteria; Actinobacteridae; Actinomycet
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01-JUN-2003 (TrEMBLrel.
Aldehyde dehydrogenase.
                                                                                                                                                                                                                               Deinococcus radiodurans.
Bacteria; Deinococcus-Thermus;
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               "Genome sequence
                               Fraser C.M.;
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(TrEMBLrel. 30, Last sequence update)
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GO; GO:0008152; P:metabolism; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR002086; Aldehyd dehydrog.
InterPro; IPR002539; MaoC_dehydratas.
InterPro; IPR01256; PaaN-DH.
Pfam; PF00171; Aldedh; 1.
Pfam; PF01575; MaoC_dehydratas; 1.
TIGR02278; PaaN-DH; 1.
Complete proteome.
SEQUENCE 700 AA; 75493 MW; E3F6FDA47;
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05-JUL-2004 ()
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EMBL; AE002069; AAF11927.1;
PIR; F75279; F75279.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
NCBI_TaxID=3345;
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NUCLEOTIDE SEQUENCE.

PubMed=14586641; DOI=10.1007/800438-003-0940-1;

PubMed=14586641; DOI=10.1007/800438-003-0940-1;

Liu J.-J., Ekramoddoullah A.K.M.;

"Isolation, genetic variation and expression of TR-NBS-LRR resistance in the pubment of the pubment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name-RGA;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
putative NBS-LRR protein C618 (Fragment).
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                                                                  Putative NBS-LRR
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GQ::0005524; F:ATP binding; IEA.
GQ::0006915; P:apoptosia; IEA.
erPro; IPR002182; NB-ARC.
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206 AA;
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                                                               (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
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3-LRR protein C605 (Fragment).
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23705 MW;
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Pred. No. 11;
1; Mismatches
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   pine)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
putative NBS-LRR protein C603 (Fragment).
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Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Strobus.
NCBI TaxID=3345;
[1]
                                                                                    NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                            Liu J.-J., Ekramoddoullah A.K.M.; "Isolation, genetic variation and expression of TIR-NBS-LRR resistance gene analogs from western white pine (Pinus monticola Dougl. ex. D.
                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; NCBI_TaxID=3345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=14586641; DOI=10.1007/s00438-003-0940-1;
                                                                                                                                                                                                                                                                                                        Name=RGA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQÜENCE
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                                                                                                                           Mol. Genet. Genomics 270:432-441(2004).
EMBL; AY294106; AAQ551158.1; -; mRNA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0006915; P:apoptosis; IEA.
InterPro; IPR002182; NB-ARC.
                                                                                                                                                                                   Don.)
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                                                                                                                                                                                                                                                                                              Pinus monticola (Western white pine).
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L; AY294107; AAQ57159.1; -; mRNA.
GO:0005524; F:ATP binding; IEA.
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206 AA;
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206 AA;
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llarity 68.8%;
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Pred. No. 11;
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                                                                                     DECF629247DB19F8 CRC64;
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Pinus; Strobus.
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RESULT 14

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Best Local S
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A Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill Brettin T.S., Bruce D., Keim P., Longmire J., Lucas S., Okinak A. Hitchock P., Jackson P., Keim P., Longmire J., Lucas S., Okinak Richardson P., Rubin E., Tice H.;

T. Complete genome sequence of Bacillus thuringiensis 97-27.";

Submirted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; AE017355; AAT60986.1; -; Genomic_DNA.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0015128; F:gluconate transporter activity; IEA.

R GO; GO:0015125; P:gluconate transporter iEA.

R InterPro; IPR003474; Glen_transporter.

R InterPro; IPR003474; Glen_transporter.

R InterPro; IPR003474; Glen_transporter.

R Complete proteome.

O SEQUENCE 250 AA; 26921 MW; 3BC16A20C586C23C CRC64;
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GGHC40 BACHK PRELIMINARY;

QGHC40;

Q6HC40;

Q5-JUL-2004 (TrEMBLrel. 27, Created)

O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)

O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)

GS-JUL-2004 (TrEMBLrel. 27, Last annotation update)

Gluconate permease, C-terminal, Gntp family.

Name=gntp; OrderedLocusNamee=BT9727 4574;

Bactilus thuringiensis (subsp. konkukian).

Bacteria, Firmicutes; Bactilales; Bactilaceae; Bactilus;
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SEQUENCE 206 AA; 23808
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Liu J.-J., Ekramoddoullah A.K.M.;
"Isolation, genetic variation and expression of TIR-NBS-LRR resistance
gene analogs from western white pine (Pinus monticola Dougl. ex. D.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Strobus.
NCBI_TaxID=3345;
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0006915; P:apoptosis; IEA.
InterPro; IPR002182; NB-ARC.
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NCBI_TaxID=180856;
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                                                                                                                Similarity 9; Conserv
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                                                                                                                                           50.5%;
                                                                                                                Score 54; DB
Pred. No. 14;
5; Mismatches
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Pred. No. 11;
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Okinaka R.,
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Search completed: March 11, 2006, 05:08:43 Job time : 132.905 secs



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C;Accession: A83785 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132 RESULT 8 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001 probable zinc-binding dehydrogenase [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text change 09-Jul-2004 A;Gene: fhuC C;Superfamily: inner membrane protein malK; ATP-binding cassette A;Cross-references: UNIPROT:Q9KDY0; UNIPARC:UPI00000C3AAF; GB:AP001510; GB:BA000004; NI A;Experimental source: strain C-125 A; Molecule type: DNA A; Residues: 1-274 <STO> A;Reference number: A83650; A;Accession: A83785 M.; Ohfuku, Y.; Funahashi, DNA Res. 5, 55-76, 1998
A;Title: Complete sequence : A;Reference number: A71000;
A;Accession: G71154 C;ACCession: G71154 R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, 밁 ş A;Molecule type: DNA A;Residues: 1-325 <KUR> A;Cross-references: UNIPROT:Q8ZAW8; UNIPARC:UPI0000DC7DA; GB:AL590842; PIDN:CAC93133.1 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AI0445 밁 ş probable adenylosuccinate synthetase - Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004 A;Cross-references: UNIPROT:058187; UNIPARC:UPI0000132805; GB:AP000002; NID:g3236129; PI A;Experimental source: strain OT3 A; Molecule type: DNA A; Residues: 1-339 < KAW > A,Status: preliminary; nucleic acid sequence not shown; translation not shown A;Statue: preliminary Species: Yersinia pestis
Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004;
Accession: AI0445 Genetics: Status: preliminary Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology; Query Match Best Local Genetics: Local Similarity 136 23 1 MAKIDNAVLPEGSLVLVTGANG 22 Similarity в ,-NIAIPEGKITTIIGANG NAVLPEGSLVLVTGANG 22 MALEDGGVTPKSGEVVVTGASG 157 Conservative Conservative 45.8%; Score 49; 50.0%; Pred. No. 46.7%; and gene organization of the genome of a hyper-thermophilic , MUID:98344137, PMID:9679194 39 ω --<u>س</u> --Score 50; Pred. No. interim Mismatches Mismatches . No. 6.4; Pyrococcus horikoshii DB 2; DB 2; 9 Length 274; 8 Length 325; for Indels Indels sequence homology 0 replaced by GenBank Gaps 0 0 ŝ Oguch: Seki

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A;Residues: 1-311 <WHI>A;Cross-references: UNIPROT:Q9RU69; UNIPARC:UPI00000D3E78; GB:AE001996; GB:AE000513; A;Experimental source: strain R1 C;Genetics:
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R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aur A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: B90054
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A;Map position: 1
C;Superfamily: ribokinase
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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C;Species: Deinococcus radiodurans
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C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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Pred. No. 15;
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Pred. No.
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T.; Zalewski,
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C;Accession: AE2904
R;Wood, D.W; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; N.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F64889
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agran
                                                                                         probable ATP-binding component of ABC transporter (PA3838) [imported] - Agrobacterium C;Species: Agrobacterium tumefaciens C;Dace: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004 C;Accession: G97679
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A; Residues: 1-264 <K
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A; Residues: 1-681 < BLAT>
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;Cross-references: UNIPROT:Q8UC28; UNIPARC:UPI00000D1FA7; GB:AE008688; PIDN:AAL43651.1
;Cross-references: UNIPROT:Q8UC28; UNIPARC:UPI0000D1FA7; GB:AE008688; PIDN:AAL43651.1
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;Experimental source: strain K-12, substrain MG1655
;301-317/Domain: transmembrane #status predicted <TM01>
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Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
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A;Gene: AGR C 4841
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library,
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C;Accession: T38115
R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream,
                                                                                                                                                                                                                                                                                                                                                                                                                probable ATP-dependent transporter - fission yeast (Schizosaccharomyces pom C;Species: Schizosaccharomyces pombe C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: G97679
A;Status: preliminary
                                                                                                                                                                                            A; Map position:
C; Superfamily: )
                                                                                                                                                                                                                                                                         A; Residues: 1-255 < CON>
A; Cross-references: UNI
                                                                                                                                                                                                                                                                                                                                       A;Reference number: Z21771
A;Accession: T38115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-264 < KI
                                                                                                                                                                                                                            A; Gene: SPDB: SPAC20G4.01
                                                                                                                                                                                                                                                          A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                         Genetics:
                                                                                                                                                                                                                                                                                                       Molecule type: DNA
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                                                                                                                                                            Query Match
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completed: March
ne : 22.254 secs
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                                                                                            9 LPEGSLVLVTGANG 22
                                                                                                                            Similarity 9; Conserv
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                                                               LPKGSRTLLVGANG
                                                                                                                                                                                            yeast hypothetical protein YFL028c; ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                              Conservative
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                11,
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                2006,
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Pred.
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Pred. No.
                05:09:45
                                                                                                                              Mismatches
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No. 15;
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17;
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                                                                                                                                                            Length 255;
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TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1932PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 32256
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TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 20894
LENGTH: 210
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APPLICANT: Alexandrov, Nickolai et al.
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GENERAL INFORMATION:
                                                                                                                                                                      Sequence 20893, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
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Best Local
APPLICANT: Alexandrov, Nickolai et al.
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 20893
LENGTH: 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(388)
OTHER INFORMATION: Ceres Seq. ID no. 13592517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1). (210)
OTHER INFORMATION: Ceres Seq. ID
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8; Conserve
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Pred. No. 26
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Pred. No.
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TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(283)
OTHER INFORMATION: Ceres Seq. ID
US-11-096-568A-1266
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; NAME/KEY: misc_feature
; LOCATION: (1)...(277)
; OTHER INFORMATION: Ceres Seq.
US-11-096-568A-20893
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SEQ ID NO 1267
LENGTH: 246
TYPE: PRT
ORGANISM: Zea mays subsp.
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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined
TITLE OF INVENTION: Therby
                                                                                                                                                                                                                                         Sequence 1266, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 1266
LENGTH: 283
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Best Local Similarity
Matches 11; Conserv
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CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
                                 Query Match
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ORGANISM:
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NAME/KEY: misc_feature
LOCATION: (1)...(246)
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nilarity 57.9%;
Conservative
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Pred. No. 21;
                   Score 41.5;
Pred. No. 26;
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L; Mismatches
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Pred. No. 22;
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RESULT 14
US-11-096-568A-12932
; Sequence 12932, Application US/11096568A
; Publication No. US20060048240A1
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US-11-052-554A-211
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US-11-096-568A-1265
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SEQ ID NO 1265
LENGTH: 316
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                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 211
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Best Local
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PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOPTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides TITLE OF INVENTION: Therby FILE REFERENCE: 2750-1592PUS2 CURRENT APPLICATION NUMBER: US/11/096,568A CURRENT FILING DATE: 2005-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYI
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays subsp. mays FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(316)
OTHER INFORMATION: Ceres Seq. ID
                                                                                                                                                                                                                                                                                    ORGANISM: Streptococcus mutans UA159
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                                                                                                                                                                                                            Match 42.3%;
Local Similarity 52.6%;
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Pred. No. 2.1e+02;
3; Mismatches 5;
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Pred. No. 30;
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Query Match
Best Local Similarity
""" hes 7; Conserve
                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10580
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10580
Search completed: March 11, 2006, 05:16:52 Job time: 11.7937 secs
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US-11-098-686-10580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10580, Application US/11098686

Publication No. US20060024696A1

GEMERAL INFORMATION:

APPLICANT: Kapur, Vivek and Gebhart, Connie J.

APPLICANT: Kapur, Vivek and Gebhart, Connie J.

TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METH
FILE REFERENCE: 09531-128001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 12932
LENGTH: 234
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                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-04
                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1) . (234)
OTHER INFORMATION: Ceres Seq.
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ORGANISM: Triticum aestivum
FEATURE:
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les 8; Conserv
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Pred. No.
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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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seq length: 0
seq length: 2000000000
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98
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425	362	362	362	346	283	252	240	240	232	206	87	511	510	510	509
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H70456	G90712	C85563	LPECRA	C81654	S41412	AH3618	A97531	AB2750	G84382	F69490	F71194	S07316	S10997	S19261	PWWTAM
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ALIGNMENTS

RESULT 1

hypothetical protein Atu3180 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004 C;Accession: AF2947 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194 A;Accession: D98335 RESULT D98335 A,Title: The Genome of the Natural Genetic A;Reference number: AB2577; MUID:21608550; A;Accession: AF2947 ; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, Lerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell ABC transporter, ATP-binding protein nmb0588 [imported] - Agrobacterium tumefaciens (str C;Species: Agrobacterium tumefaciens C;Date: 22-Oct_2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004 밁 á A; Experimental source: strain C58 A; Molecule type: DNA A; Residues: 1-277 < KUR> ster, E.W. A;Cross-references: C;Genetics: C; Accession: D98335 A; Map position: linear chromosome A;Gene: Atu3180 A;Status: preliminary A;Gene: AGR_L_3258 A;Map position: linear chromosome A; Molecule type: DNA A; Residues: 1-277 < KUR> A; Status: preliminary Cross-references: UNIPROT:Q8UB37; UNIPARC:UPI0000D20E7; GB:AE008689; Best Local Similarity Matches 10; Conserv Genetics: Query Match 25 4 DGATARGSLTAVVGANG DNAVLEGSLVKVTGANG 20 Conservative UNIPROT: Q8UB37; 52.0%; 58.8%; 41 Score 51; I Pred. No. 1 (Dupont) UNIPARC: UPI00000D20E7; GB:AE007870; PIDN:AAK90206.1; Mismatches Agrobacterium tumefaciens (strain C58, Engineer Agrobacterium tumefaciens C58 PMID:11743193 DB 1.5; 2 6, Length 277; Indels °, Gaps PIDN: AAL43996.1; 0 Dupont)

S24761 A46230 T08588 S29876 S29876 A69415 A69415 S46508 S12309 PWZMAM S12309 PWZMAM S269792 S269792 S269792 S269792 PWRZAM

probable H+-transp H+-transporting tw conserved hypothet H+-transporting tw
RNA-binding protei hypothetical prote

prote

Cpo 61.1

protein

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A;Status: p.c......
A;Molecule type: DNA
A;Mesidues: 1-592 <STO>
A;Cross-references: UNIPROT:Q9HYS1;
A;Cross-references: strain PAO1
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                RESULT 5
AF2697
                                                                                                                                                                                                                                A; MOLECULE 'JF' A; Residues: 1-636 <PAR>
A; Residues: 1-636 <PAR>
A; Cross references: UNIPROT: Q9JVX3;
A; Cross references: gerogroup A,
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A;Molecule type: DNA
A;Residues: 1-636 <PAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, ar
two component
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Best Local :
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50; MUID:20437337; PMID:10984043
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Pred. No. 11;
1; Mismatches
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strain Z2491
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No. 7.

    Agrobacterium tumefaciens

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A.; Larbig,
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K.; Lim,
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                            A,Title: Genome sequence of enterohemorrhagic Escherichia A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: D85608
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                A;Status: preliminary
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AF2697
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Cher erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li; Karp, P.; Romero, P.; Zhang, S. science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent A;Reference number: A97359; MUID:21608551; PMID:11743194 A;Accession: F97479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Goodner, B.; Hinkle, G.; Gattung, S.;
A.; Liu, F.; Wollam, C.; Allinger, M.;
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-motile and phage-resistance protein [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004 C;Accession: F97479
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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A; Residues: 1-778 < KUR>
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A; Residues: 1-778 < KUR>
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Doughty, D.; Scott, C.; Lappas, C.; Markelz,
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ckelz, B.;
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D.J.; Mayhew K.; Apodaca,

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A;Residues: 1-111 <STO>
A;Cross-references: UNIPROT:Q8X9P2; UNIPARC:UPI00000D07CC; GB:AE005174; NID:g12513991;
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Cha Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to Genfank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-111 <ST2>
                                                                                                                                                                                                                                                                                                              hypothetical protein aq 294 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: H70326
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                                                                                                                                                                                               A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: H70326
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A;Accession: D90218
                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not
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A;Residues: 1-181 <KUR>
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A; Residues: 1-371 < AQF >
                                                                                                                                                                                                                                                        Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                              R;Deckert, G.; Warren, P.V.; Gaasterland,
                                                                                                                     A;Cross-references: UNIPROT:066644; UNIPARC:UPI00000562FF; GB:AE000682; NID:g2982979;
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Best Local Similarity
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47.6%; Pred. No.
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R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, submitted to the Protein Sequence Database, March 1999
                                                                                             RESULT 12
A32687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein W03D8.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change
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A;Experimental source: cultivar Columbia; BAC clone T28I19
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           lysyl endopeptidase (EC 3.4.21.50) precursor - Achromobacter N;Alternate names: Achromobacter proteinase I C;Species: Achromobacter lyticus C;Species: Achromobacter lyticus C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_chan C;Accession: A32687; A32960
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A;Introns: 47/1; 82/3; 115/1; 230/1; 319/2; 406/3; 466/1; 513/1; 554/2;
                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-1647 <JON>
A;Cross-references: UNIPARC:UPI0000164013; EMBL:AF043702;
A;Experimental source: strain Bristol N2; clone W03D8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Jones, K.; Graves, T.; Ozersky, P.
submitted to the EMBL Data Library, January 1998
A;Description: The sequence of C. elegans cosmid WO3D8
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A; Map position:
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A; Residues: 1-532 <BEV>
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                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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R;Ohara,
                                                                                                                                                                                                                         Query Match
Best Local S
Matches 10
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9; Conserv
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 K.; Shinagawa,
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83.3%;
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Pred. No.
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Pred. No.
 H.; Nakata,
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66;
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   A.; Norioka,
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                               #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                            Length 1647;
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     S.; Sakiyama, F.
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RNA-binding protein homolog Cpo (clone 61.2) - fruit fly (Drosophila melanogaster) N;Alternate names: couch potato protein 61.2; cpo61.2 protein (C;Species: Drosophila melanogaster C;Date: 21-Sep-1993 #sequence_revision 30-Apr-1999 #text_change 15-Mar-2004 C;Accession: B46230; S24678 C;Accession: B46230; S24678 R;Bellen, H.J.; Kooyer, S.; D'Evelyn, D.; Pearlman, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 264, 20625-20631, 1989

A;Title: Cloning, nucleotide sequence, and expression of Achromobacter protease I gene. A;Reference number: A32687; MUID:90062204; PMID:2684982

A;Accession: A32687

A;Accession: A32687

A;Molecule type: DNA

A;Residues: 1-653 < CHA>

A;Cross-references: UNIPROT:P15636; UNIPARC:UPI0000125C8B; GB:J05128; NID:g141803; PIDN

A;Cross-references: UNIPROT:P15636; UNIPARC:UPI0000125C8B; GB:J05128; NID:g141803; PIDN

A;Tsunasawa, S.; Masaki, T.; Hirose, M.; Soejima, M.; Sakiyama, F.

J. Biol. Chem. 264, 3832-3839, 1989

A;Title: The primary structure and structural characteristics of Achromobacter lyticus

A;Reference number: A32960; MUID:89139439; PMID:2492988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: CESP:D2063.1
A;Map position: 5
A;Introns: 294/3; 373/3
A;Introns: 294/3; 359/3; 373/3
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology C;Keywords: NAD; oxidoreductase; zinc C;Keywords: NAD; oxidoreductase; zinc F;47,70,173/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-408 <BEC>
A;Cross-references: UNIPROT:Q9UAT1; UNIPARC:UPI00000762B1; EMBL:AF125951; PIDN:AAD14690.
A;Experimental source: strain Bristol N2; clone D2063
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable alcohol dehydrogenase (EC 1.1.1) [similarity] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004 C;Accession: T33939 R;Becker, M.; Graves, T.; Wilson, C. submitted to the EMBL Data Library, February 1999 A;Description: The sequence of C. elegans cosmid D2063. A;Reference number: Z21442 A;Accession: T33939
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F;21-205/Domain: propeptide #status predicted PRO>
F;21-205/Domain: propeptide #status predicted PRO>
F;206-473/Product: achromobacter proteinase I #status experimental <MAT>
F;211-421,217-285,241-263/Disulfide bonds: #status experimental
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C;Comment: This protein specifically hydrolyzes lysyl peptide bonds including
C;Keywords: hydrolase; serine proteinase
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A;Residues: 206-473 <TSU>
A;Cross-references: UNIPARC:UPI000011061E
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Best Local
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Pred. No. 29;
3; Mismatches
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Pred. No. 21;
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A;Molecule type: DNA
A;Residues: 1-536 <BEL>
A;Cross-references: UNIPARC:UPI000017BECA; GB:Z14312
A;Note: sequence extracted from NCBI backbone (NCBIN:117907, NCBIP:117908)
R;Bellen, H.J.
                                                                                                                                                                                                                      A;Gene: FlyBase:cpo
A;Cross-references: FlyBase:FBgn0000363
A;Crtart codon: CTC
A;Introns: 450/1; 475/1; 493/3; 514/3; 562/1
F;452-520/Domain: ribonucleoprotein repeat homology <RRM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: FlyBase:cpo
A;Start codon: CTC
C;Keywords: alternative splicing; RNA binding
F;453-521/Domain: ribonucleoprotein repeat homology
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A;Accession: B46230
A;Status: preliminary
Search completed: March 11, 2006, 05:09:43 
Job time : 20.4127 secs
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A; Residues: 1-615 <BEL>
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 15-Mar-2004
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Matches 9; Conserv
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75.0%;
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75.0%;
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Pred. No.
                                                                                                                                                                     Score 45;
Pred. No.
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A Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.
A Tang M., Lopez de Leon A., Xiang H., Gusti V., Clausen I.G.,
A Clsen P.B., Rasmussen M.D., Andersen J.T., Joergensen P.L.,
A Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N.,
A Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N.,
A Chromit S.D., Berka R.M.,
A Chomplete genome sequence of the industrial bacterium Bacillus
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QGSDJ1; QG62P10;

25-OCT-2004 (TYEMBLrel. 28, Created)

25-OCT-2004 (TYEMBLrel. 28, Last sequence update)

13-SEP-2005 (TYEMBLrel. 31, Last annotation update)

YWDD (SAM (And some other nucleotide) binding motif, PUA of the public of the publ
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PubMeda15383718; DOI=10.1159/000079829;
Veith B., Herzberg C., Steckel S., Feess
Ehrenreich P., Baeumer S., Henne A., Li
Ehrenreich A., Gottschalk G.;
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SEQUENCE
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01-OCT-2000 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
F1 ATPase alpha subunit
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Q9MM39;
01-OCT-2000 (TrEMBLrel. 1
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J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
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Spermatophyta; Gnetophyta;
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         NUCLEOTIDE SEQUENCE.
MEDLINE=20226063; PubMed=10760278;
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Pred. No.
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., Liesegang
             DOI=10.1073/pnas.97.8.4092
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Gnetales; Gnetaceae; Gnetum
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H., Merkl R.,
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GO; GO:0015992; P:proton transport; IEA.

DR InterPro; IPR005294; ATP_synthF1_alph.

DR InterPro; IPR004100; ATPase a/b N.

DR InterPro; IPR004104; ATPase a/b N.

DR InterPro; IPR004104; ATPase a/b centre.

Pfam; PF00006; ATP-synt_ab; 1.

DR Pfam; PF02874; ATP-synt_ab; 1.

DR TIGRFAMS; TIGR00962; atph. 1.

DR TIGRFAMS; TIGR00962; atph. 1.

RW ATP Synthesis; ATP-binding; CF(1); Hydrogen ion transport; Hydrolase; MON_TER 1.

FT NON_TER 412 412

SQ SEQUENCE 412 AA: 47000
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Q9T7A3 GN
ID Q9T7
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          DR RAY DR
MUCLEOTIDE SEQUENCE.

MEDLINE=20052162; PubMed=10586879; DOI=10.1038/46536;

X QUI Y.L., Lee J., Bernasconi-Quadroni F., Soltis D.E., Solt Qui Y.L., Lee J., Bernasconi-Quadroni F., Soltis D.E., Solt Qui Y.L., Lee J., Bernasconi-Quadroni F., Soltis D.E., Solt Qui Y.L., Lee J., Bernasconi-Quadroni F., Soltis D.E., Soltis M.W.;

The earliest angiosperms: evidence from mitochondrial, plating 402:404-407(1999).

Lacture 402:404-407(1999).

REMBL; P19463; 1E79.

REMBL; P19463; 1C:proton-transporting ATP synthase complex GO; GO:0005739; C:mitochondrion; IEA.

RGO; GO:0016469; C:proton-transporting two-sector ATPase complex GO; GO:0016469; C:proton-transporting ATP synthase activ.

RGO; GO:0016433; F:ATP binding; IEA.
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Proc. Natl. Acad. Sci. U.S.A. 97:4092-4097(2000).

-I- SIMILARITY: Belongs to the ATPase alpha/beta chain EMBL; AF209109; AAF64667.1; -; Genomic_DNA.

HSSP; P19483; 1H8E.

SMR: COAMTA
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
ATPase alpha subunit (Fragme
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Q9T7A3;
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Spermatophyta; Gnetophyta; Gnetopsida; Gnetales; Gnetaceae; Gnetum
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GO:0005739; C:mitochondrion; IEA.

GO:0005739; C:mitochondrion; IEA.

GO:0016451; C:proton-transporting ATP synthase complex, C:

GO:0016469; C:proton-transporting two-sector ATPase comple

GO:0005524; F:ATP binding; IEA.

GO:0046931; F:hydrogen-transporting ATP synthase activity.

GO:0046961; F:hydrogen-transporting ATPase activity, rota.

GO:0016787; F:hydrolase activity, acting on acid anhydrid.

GO:0016820; F:hydrolase activity, acting on acid anhydrid.

GO:0016986; F:ATP synthesis coupled proton transport; IEA.

GO:0016811; F:ion transport; IEA.
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R GO; GO:0016911; P:ion transport; IEA.

R GO; GO:0016912; P:proton transport; IEA.

R GO; GO:0016992; P:proton transport; IEA.

R GO; GO:0015993; ATP synther alph.

R InterPro; IPR000793; ATPase=a/b_C.

R InterPro; IPR000194; ATPase=a/b_N.

R InterPro; IPR000194; ATPase=a/b_C.

R InterPro; IPR000194; ATPase=a/b_C.

R InterPro; IPR000194; ATPase=a/b_C.

R InterPro; IPR000194; ATPase=a/b_C.

R Ffam; PF00006; ATP-synt_ab; 1.

R Pfam; PF00306; ATP-synt_ab; 1.

R Pfam; PF00306; ATP-synt_ab; 1.

R Pfam; PF02874; ATP-synt_ab; 1.

R Pfam; PF030152; ATPASE ALPHA BETA; 1.

R PROSITE; PS00152; ATPASE ALPHA BETA; 1.

R PNON_TER 418 AA. 4475 MW. OFFESSABRS722901 CRC64.
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Best Local
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Q691P6;
Q691P6;
                                                                                                                                                                                                                                                                                                                                                  PROSITE;
SEQUENCE
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Submitted (MAR-2004) to the EMBL/G EMBL; AP006753; BAD32124.1; -; Gen Gramene; Q69IP6; -
QARSV8_TETNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative aspartic proteinase nepenthesin I.
                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0004194; F:pepsin A activity; GO; GO:000508; P:proteolysis and pep InterPro; IPR001461; Peptidase_A1. InterPro; IPR001969; Pept_Asp_AS. Pfam; PF00026; Asp; 1. PRINTS; PR00792; PEPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=OSJNBa0039D04.13;
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                             8
TETNG
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                                                                                                                                                                                                                                                                       Similarity
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451 AA; 46440 MW; I
                                                                                                                                                                                           DNAVLEGSLVKVTGAN 19
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                                                                                                                                       DSPILFGSLAKVTGGN
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Pred. No. 48;
4; Mismatches
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                                                                                                                                                                                                                                           Score 50; DB
Pred. No. 51;
2; Mismatches
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-; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yose Y.;
genomic DNA,
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E7F24FED78353C5E CRC64;
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          PRT;
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A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
A Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
A Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
A Anthouard V., Jubin C., Castelli V., Boudet N., Castellano S.,
A Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
A Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
A Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
A Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
A Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
A Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
A Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
A Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
A Laudet V., Schacher V., Quetter F., Saurin W., Scarpelli C.,
A Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
"The early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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NON TER
SEQUENCE
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Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Verte
Eukaryota; Metazoa; Chordata; Craniata; Verte
Actinopterygii; Neopterygii; Teleostei; Eutel
Acanthomorpha; Acanthopterygii; Percomorpha;
Tetradontoidea; Tetraodontidae; Tetraodon.
Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruv
                                                                                                                                                                                                                                                                                                                                                                                                  Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
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25-OCT-2004 (TriMBLrel. 28, Last sequence update)
25-OCT-2004 (TriMBLrel. 28, Last annotation update)
5imilar to CA1657 | IPF16022 Candida albicans IPF16022 unknown
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13-SEP-2005 (TrEMBLrel.
13-SEP-2005 (TrEMBLrel.
Chromosome 12 SCAF14999)
                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC | STRAIN=ATCC 36239 / CBS 767; PubMed=15229592; DOI=10.1038/nature02579;
                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales;
NCBI_TaxID=4959;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q6BIS4;
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Submitted (FEB-2004) to the
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TER 687 6
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, Aury J.M., Brunet
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; 72523 MW;
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31, Last sequence upda
31, Last annotation up
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Euteleostei; Neoteleostei;
rpha; Tetraodontiformes;
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WE RESERVE TO THE PROPERTY OF 
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GO; GO:0004312; F:fatty-acid synthase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:000613; P:fatty acid biosynthesis; IEA.
GO; GO:000613; P:metabolism; IEA.
GO; GO:0008152; P:metabolism; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR004136; 2nprop_dioxygen.
InterPro; IPR004136; 2nprop_dioxygen.
InterPro; IPR003965; Fatty_acid_synth.
R Ffam; PF00109; Ketoacyl_synth.
R Pfam; PF002801; Ketoacyl_syntc; 1.
R Pfam; PF02801; MaoC_dehydratas; 1.
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Best Local
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EMBL; CR382139; CAG90360.1; -; Genomic_DNI
InterPro; IPRO01680; WD40.

Pfam; PF00400; WD40; 6.

SMART; SM00320; WD40; 6.

PROSITE; PS50294; WD REPEATS REGION; 1.

Complete proteome; Repeat; WD repeat.

SEQUENCE 1048 AA; 117153 MW; 7BAEB602;
                                                                                                                                                                                                                                                                                                                                     Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Muller H., Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A., Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Wincker P., Souciet J.-L.; "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002)
EMBL; AE014295; AAN25329.1; -; Genomic_DNA.
HSSP; P25715; 1MLA.
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QBG456;
Q1-MAR-2003 (TrEMBLrel. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-22294977; PubMed-12381787; DOI-10.1073/pnas.212527599; Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE STRAIN=NCC 2705;
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Bifidobacteriaceae; Bifidobacterium.
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                   PRINTS; PRO1483; FASYNTHASE.
PROSITE; PS00606; B_KETOACYL_SYNTHASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The
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Last annotation updat
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Pred. No. 1.2e+02;
4; Mismatches 5
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STRAIN=ATCC 15692 / PAO1;

STRAIN=ATCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;

MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;

MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Weetbrock-Wadman S., Yuan Y.,

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Garber R.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Smith K.A., Spencer D.H., Jr., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                           Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                 Pfam; PF00561; Abhydrolase 1; 1.
Pfam; PF00106; adh short; 1.
PRINTS; PR00412; EPCXHYDRLASE.
PRINTS; PR00081; GDHRDH.
PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
                                                                                                                                                                                                                                                                                           EMBL; AE004754; AAG06712.1; -; Ge
PIR; B83231; B83231.
HSSP; Q7Z4W1; 1PR9.
GO; GO:0016491; F:oxidoreductase
GO; GO:0008152; P:metabolism; IEP
                                                                                                                                                                                                                                                                                                                                                                Reizer J., Saier M.H. Jr., Hancock R.E.W., Lory S., "Complete genome sequence of Pseudomonas aeruginosa opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa
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                                                                                                                                                                                                                                    InterPro; IPR000073; A/b hydrolase.
InterPro; IPR002198; AM short.
InterPro; IPR002147; Adh short C2.
InterPro; IPR000639; Epox_hydrolase.
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592 AA;
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PDASSMNGKLVVVTGAGG
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Pred. No. 3.
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Pred. No.
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RESULT 12
Q4ZUU5_PSESY
ID Q4ZUU5_PSESY PRELIMINARY; PRT; 732 AA.
AC Q4ZUU5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DT 01-SEP-2005 (TrEMBLrel. 31, Last annotation update)

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PESULT DNL PS ID I DN AC P5 AC
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Matches 10; Conserv
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SIGNAL
                                                                                                                                                                             NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF N-TERMINUS STRAIN=VG1 / DSM 3638 / ATCC 43587 / JCM 8422; Mathur E.J., Marsh E.J., Schoettlin W.E.; "Purified thermostable Eyrococcus furiosus DNA ligase." Patent number US5700672, 23-DEC-1997.
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P56709;
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InterPro; IPR003991; Pertactin C.
Pfam; PF03797; Autotransporter; 1.
Pfam; PF03212; Pertactin; 1.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-2005) to the EMBL/GenBank/DDBJ EMBL; CP000075; AAY37077.1; -; Genomic_DNA. InterPro; IPR005546; Auto_transptbeta. InterPro; IPR006315; Autotransporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chain P., Larimer F., DiBartolo G., Copeland A., Lykidis A., Trong S., Nolan M., Goltsman E., Thiel J., Malfatti S., Lapidus A., Detter J.C., Land M., Richardson P.M., Kyrpides N.C., Ivanova N.;

Land M., Richardson P.M., Kyrpides N.C., Ivanova N.;

"Comparison of two complete genome sequences of Pseudomonas syringae pv. syringae B728a and pv. tomato DC3000.";

Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2005).
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                        NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRALN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYRFU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=lig; OrderedLocusNames=PF1635;
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75763 MW;
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Pred. No. 1.2e
1; Mismatches
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DT 25-OCT-2
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DT 25-OCT-2
DT Alcohol
GN Name=adh
OS Leifsoni
OC Bacteria
OC Micrococo
OX NCBI_Tax
RN [1]
RP NUCLEOTI
RC STRAIN-C
RX PubMed-1
RA Monteiro
RA Mineida
RA Almeida
RA Ferro M.
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R HAMAP; ME 00407; -; 1.

RINTERPRO; IPR010307; DNA ligase A C.

InterPro; IPR012309; DNA ligase A C.

InterPro; IPR012310; DNA ligase A M.

InterPro; IPR012310; DNA ligase A M.

InterPro; IPR012310; DNA ligase A M.

InterPro; IPR012308; DNA ligase A C; 1.

R InterPro; IPR012310; DNA ligase A C; 1.

R Pfam; PF04679; DNA ligase A C; 1.

R Pfam; PF01068; DNA ligase A N; 1.

R Pfam; PF01068; DNA ligase A N; 1.

R Pfam; PF01068; DNA ligase A N; 1.

R Pfam; PF0475; DNA ligase A N; 1.

R Pfam; PF04675; DNA Ligase A; 1.

R PROSITE; PS00697; DNA LIGASE A2; FALSE NEG.

R PROSITE; PS00333; DNA LIGASE A3; 1.

ATP-binding; Cell CyCle; CDNA damage; DNA recombination; DNA DNA replication; Ligase; Nucleotide-binding.

DNA replication; Ligase; Nucleotide-binding.

ACT_SITE 249 249 No.-AMP-lysine intermediate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Monteiro-Vitorello C.B., Camargo L.B.A., Van Sluys M.A., Kitajima J.P., Truffi D., do Amaral A.M., Harakava R., de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y., Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte Almeida N.F. Jr., Carrer H., Coutinho L.L., El-Dorry H.A., Ferro M.I.T., Gagliardi P.R., Giglioti E., Goldman M.H.S., Goldman G.H., Kimura E.T., Ferro E.S., Kuramae E.E., Lemos E.G.M.,
                                                                                                                                                                                                                                            Leifsonia xyli (subsp. xyli)
Bacteria; Actinobacteria; Ac
Micrococcineae; Microbacteri
                                                                                                                                   STRAIN=CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                  PubMed=15305603;
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RESULT 15

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O1-OCT-2001 (TrEMBLrel. 18, Last sequence update)
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O1-OCT-2001 (TrEMBLrel. 18, Last sequence update)
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O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DT
O2-Carboxypeptidase.
OX
OARCHAGAS; BUTYARCHAGOTA; Thermoplasmata; Thermoplasmatal
OC Thermoplasmataceae; Thermoplasma.
OX
NCBI_TAXID=5039;

RN
UCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RC STRAIN=GSS1 / DSM 4299 / JCM 9571;
RC STRAIN=GSS1 / DSM 4299 / JCM 9571;
RA KAWASHIMA T., AMADON N. KOIKe H., MAKIMO S.-I., Higuchi
RA KAWASHIMA T., AMADON N. KOIKe H., MAKIMO S.-I., Higuchi
RA KAWASHIMA T., YAMADON Y., KATAMAKI H., MAKIMO S.-I., Higuchi
RA KAWASHIMA T., AMADON Y., ATAMAKI H., MAKIMO K., SUZUK
RT "Archaeal adaptation to higher temperatures revealed by
RT sequence of Thermoplasma volcanium.";
RIC POC. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
DR EMBL; BAD00001; BAB59893.1; -; Genomic_DNA.
DR GO; GO:0006508; -:
CO GO:0006508; -:
CO GO:0006508; F:proteclysis and peptidase activity; IEA.
DR GO; GO:0006508; F:proteclysis and peptidolysis; IEA.
DR GO; GO:0006508; F:proteclysis and peptidolysis; IEA.
DR GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
DR GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
DR GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
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R GG; GO:0004180; F:carboxypeptidase activity; IEA.

R GG; GO:0016787; F:hydrolase activity; IEA.

R GG; GO:0016787; F:metallopeptidase activity; IEA.

R GG; GO:0008237; F:metallopeptidase activity; IEA.

R GG; GO:0006598; F:protechydisis and peptidolysis; IEA.

R GG; GO:0006508; P:protechydisis and peptidolysis; IEA.

R InterPro; IPR011650; M20 dimer.

R InterPro; IPR0102933; Peptidase_M20.

R Pfam; PF07687; M20 dimer; 1.

R Pfam; PF07687; M20 dimer; 1.

R Pfam; PF01546; Peptidase_M20; 1.
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Mol. Plant Microbe Interact. 17:827-836(2004).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
EMBL, ABO16822; AAT08202.1; -; Genomic DNA.
GO; GO:0016491; F:oxidoreductase activIty; IEA.
GO; GO:0018270; F:zinc ion binding; IEA.
InterPro; IFR002085; ADH_Sir_D.
Pfam; pF00107; ADH_zinc_N; I.
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STRAIN-GSS1 / DSM 4299 / JCM 9571;
MEDLINE-20570466; PubMed-11121031; DOI=10.1073/pnas.97.26.14257;
KAWASHIMA T., AMANO N., KOİKE H., MAKİNO S.-I., HİGUCHİ S.,
KAWASHIMA-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamot
Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
Warchaeal adaptation to higher temperatures revealed by genomic
sequence of Thermoplasma volcanium.";
Broc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
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Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
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    261
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                                                                             N
                                                                                                                                                                   l Similarity
9; Conserve
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                                                                                                                                                                                                                                                                                                                                                    4D6BBE73321C7327 CRC64;
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Kawamoto T.,
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sporobolomyces salmonicolor ketoreductase, aldehyde reductase II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method of preparing high yields of an (R)-hydroxy ester by reducing an alpha-keto ester using a ketoreductase enzyme. The present sequence represents Sporobolomyces salmonicolor ketoreductase, aldehyde reductase II used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (R)-hydroxy ester; alpha-keto ester; ketoreductase;
aldehyde reductase II.
                                                                                                                                                                                                                                           Sporobolomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 343 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 3; 10pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Preparing (R)-hydroxy ester involves adding alpha-keto ester comprising ketoreductase enzyme and non-ketoreductase enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moore JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUL-2003; 2003US-00616320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-AUG-2004
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(STUR/) STURR M G.
(MCLA/) MCLAUGHLIN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JUL-2002; 2002US-0394761P
                                                                       US2004101937-A1
                                                                                                                                                                    (R)-hydroxy ester;
aldehyde reductase
                                                                                                                        Sporidiobolus salmonicolor
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                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                           salmonicolor aldehyde
                                                                                                                                                                                                                                                                                                                                                                                           peptide; 21
                                                                                                                                                                      alpha-keto
II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 107; DB 8;
100.0%; Pred. No. 2.2e-08;
ative 0; Mismatches 0;
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                                                                                                                                                                                                                                           reductase II, N-terminal peptide
                                                                                                                                                                                                ketoreductase;
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                                                                                                                                                                                                enzyme;
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Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of preparing high yields of an (R)-hydroxy ester by reducing an alpha-keto ester using a ketoreductase enzyme. The present sequence represents a Sporobolomyces salmonicolor ketoreductase, aldehyde reductase II, N-terminal peptide used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preparing (R)-hydroxy ester involves adding alpha-keto ester to mixture comprising ketoreductase enzyme and non-ketoreductase enzyme components.
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(STUR/)
                                                                                                       (MOOR/)
(STUR/)
(MCLA/)
(KIMJ/)
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                                                                                                                                                                                                                                    Sporidiobolus salmonicolor
                                                                                                                                                                                                                                                        aldehyde
                                                                                                                                                                                                                                                                                   Sporobolomyces salmonicolor aldehyde reductase II, N-terminal
                                                                                                                                                                                                                                                                                                                                             ADO56194 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moore JC, Sturr MG,
                                   Preparing (R)-hydroxy ester involves adding alpha-keto ester to mixture comprising ketoreductase enzyme and non-ketoreductase enzyme components.
                                                                                    Moore
                                                                                                                                                       10-JUL-2002; 2002US-0394761P
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                  Claim 1; SEQ
                                                                  WPI; 2004-431257/40.
                                                                                                                                                                                                                                                                 (R) -hydroxy ester;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Similarity
                                                                                                       ) MOORE J C.
) STURR M G.
) MCLAUGHLIN
) KIM J.
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                                                                                                                                                                                                                                                        reductase
                                                                                     Sturr MG,
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                  ID NO 1; 10pp; English
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                                                                                                                                                                                                                                                         alpha-keto ester; ketoreductase; enzyme
II.
                                                                                                                                                                                                                                                                                                                                                                                                                                             64.0%;
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                                                                                      Mclaughlin K,
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Pred. No. 0.0011;
0; Mismatches
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The invention relates to a method of preparing high yields of an

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promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nitrogen;
bacterial
                                                                                                                                                                                                                                            New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hydroxy ester by reducing an alpha-keto ester using a ketoreductase enzyme. The present sequence represents a Sporobolomyces salmonicolor ketoreductase, aldehyde reductase II, N-terminal peptide used in the method of the invention.
                                                                                                                                                                                      The invention relates to a recombinant DNA construct comprising
                                                                                                                                                                                                                 Claim 1; SEQ ID NO 14080; 122pp;
                                                                                                                                                                                                                                                                                                                                                                         (CAOY/)
(HINK/)
(SLAT/)
(CHEN/)
(GOLD/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria
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                                                                                                                                                                                                                                                                                                                                                                          GOLDMAN
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polypeptide.
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14-NOV-1997;
18-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
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14-JAN-1998;
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Pred. No.
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N. gonorrhoeae antigenic proteins. They are encoded by open reading frames (ORFs) AAZ11972-Z12358. The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense

(as

Amino acid sequences AAY38499-Y38944 represent Neisseria meningitidis and

diagnosis,

Claim 4; Page

336; 524pp; English.

Proteins from Neisseria meningitidis and N. gonome diagnosis, treatment and prevention of infection.

gonorrhoeae useful for

1999-327407/27.

Sequence

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Best Local Similarity 47.4%;
                                                                                                         Amino acid sequences AAY38499-Y38944 represent Neisseria meningitidis and N. gonorrhoeae antigenic proteins. They are encoded by open reading frames (ORFs) AAZ11972-Z12358. The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septiceemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense
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                                                                              Sequence 461 AA;
                                                                                                                                                                                         Claim 4; Page 336; 524pp; English.
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VDGALAPACSVILITGAGG
                 IDNAVLPEGSLVLVTGANG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                            gonorrhoeae.
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97GB-00024190.
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97GB-00026147.
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                                                                                                                                                                                                                                                                                                                                                   The present sequence represents the amino acid sequence of a N. gonorrhoeae protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6914131B1.
                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid molecule. The methods and compositions of the present invention are useful for diagnosing and/or treating Neisserial bacterial infections, in particular meningitis and septicemia caused by Neisseria meningitidis and Neisseria gonorrhea.
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                                             antibacterial; immunosuppressive; antiinflammatory; vaccine; neisseria gonorrhoeae infection; gynecological; infection; neisseria meningitidis infection; meningitis; neuroprotective;
                                                                                             N. gonorrhoeae protein SEQ ID NO 590.
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                               Disclosure; Page 257;
                                                                            New protein from Neisseria medicament for treating or
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                                                                       Amino acid sequences AAY38499-Y38944 represent Neisseria meningitidis and N. gonorrhoeae antigenic proteins. They are encoded by open reading frames (ORPs) AAZ11972-Z12358. The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense
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                                                                                                                                      Sequence 461 AA;
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27-NOV-1997;
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                                                                                                              The invention relates to an isolated nucleic acid molecule. The methods and compositions of the present invention are useful for diagnosing and/or treating Neisserial bacterial infections, in particular meningitis and septicemia caused by Neisseria meningitidis and Neisseria gonorrhea. The present sequence represents the amino acid sequence of a N. meningitidis protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibacterial; immunosuppressive; antiinflammatory; vaccine; neisseria gonorrhoeae infection; gynecological; infection; neisseria meningitidis infection; meningitis; neuroprotective;
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US-09-543-681A-6546
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LENGTH: 687
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
S-09-489-039A-13937
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GENERAL INFORMATION:
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LENGTH: 340
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Patent No. 6605709
GENERAL INFORMATION:
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CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.2004001
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PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: 60/152,318
PRIOR FILING DATE: 1999-09-03
                                 APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
FRIOR APPLICATION NUMBER: US 60/128,706
RRIOR APPLICATION NUMBER: US 60/128,706
RRIOR FILING DATE: 1999-04-09
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CURRENT APPLICATION NUMBER: US/09/605,703B
CURRENT FILING DATE: 2000-06-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zelder, Öskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORVNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
TITLE OF INVENTION: PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Corynebacterium glutamicum
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les 8; Conserv
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42.9%; Pred. No. 9.4;
tive 4; Mismatches
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27987
LENGTH: 675
TYPE: PRT
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US-09-543-681A-6546
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Best Local Similarity
"hes 9; Conserve
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MARC J. RUBENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Applic
Patent No. 6132968
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                                                     ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIA Release #1.0, V
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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TYPE: PRT
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APPLICANT: Weinfeld, Michael
APPLICANT: Xing, James Z
                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
CORRESONDENCE ADDRESS:
ADDRESSES: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                      APPLICANT: Xing, James Z.
TITLE OF INVENTION: Methods for Quantitating Low Level
TITLE OF INVENTION: Modifications of Nucleotide Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity nes 11; Conserv
APPLICATION NUMBER: FILING DATE: 13-MAY CLASSIFICATION: 435
                                                                                                                                                                                                        CITY: San Francisco
STATE: California
                                                                                                                                                                                      COUNTRY:
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61.1%;
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Pred. No. 46;
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Pred. No. 28;
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                                                                              Version #1.30
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US-09-650-855-101
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TYPE: PRT
; ORGANISM: Escherichia coli
US-09-651-656-101
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US-09-651-656-101
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         GENERAL INFORMATION:
APPLICANT: MCCUTHEN-MALONEY, SANDRA
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
APPLICANT: LAWRENCE CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA
TITLE OF INVENTION: MUTATIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND DNA
TITLE OF INVENTION: MISMATCHES
FILE REFERENCE: LI-10284
CURRENT APPLICATION NUMBER: US/09/650,855
CURRENT APPLICATION NUMBER: 08/09/650,855
CURRENT FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: 60/192,764
PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 106
                                                                                                                                                                                                                                   Sequence 101, Application US/09650855 Patent No. 6365355
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Patent No. 634050
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PRIOR FILING DATE: 2000-0
NUMBER OF SEQ ID NOS: 106
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CURRENT APPLICATION NUMBER: US/09/651,656
CURRENT FILING DATE: 2000-08-29
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APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
TITLE OF INVENTION: DETECTION AND QUANTITATION OF SINGLE NUCLEOTIDE
TITLE OF INVENTION: POLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTATIONS,
TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
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MOLECULE TYPE:
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LENGTH: 940 amino acids
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PatentIn Ver.
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Pred. No. 1e+02;
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Pred. No. 1e+02;
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Best Local Similarity
Watches 8; Conserve
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US-09-489-039A-8607
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US-09-489-039A-8607
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US-09-650-855-101
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                                                                                                                                          US-09-134-000C-3792
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GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

FILE REFERENCE: 2709.2004001
                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: LYNN DOUGETTE-Stamm et al
APPLICANT: LYNN DOUGETTE-STAMM et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 022796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR PILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 3792
LENGTH: 111
TYPE: PRT
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CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8607
LENGTH: 941
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Best Local :
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                                                                                                                                                         ORGANISM: Enterococcus faecalis
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8; Conserve
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                                 4 IDNAVLPEGSLVLVTG 19
                                                                  Similarity 9; Conserv
VDPSVIPLGSLVKVSG
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ilarity 47.1%;
Conservative
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llarity 56.2%;
Conservative
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Pred. No.
                                                                    Score 45; DB pred. No. 10; 4; Mismatches
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Pred. No. 1e+02;
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10;
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Search completed: March 11, 2006, 05:11:14 Job time : 31.0317 secs

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US-10-616-320A-1
                                                                                                                                              RESULT 9
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APPLICANT: Jefferey C. Moore
APPLICANT: Michael G. Sturr
APPLICANT: Kathleen McLaughlin
APPLICANT: Jachon Kim
APPLICANT: Jachon Kim
APPLICANT: Jachon Kim
APPLICANT: Jachon Kim
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10616320A Publication No. US20040101937A1
Sequence 14080, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENCTH: 20
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                 Query Match
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APPLICANT: Michael G. Sturr
APPLICANT: Kathleen McLaughl
APPLICANT: Jaehon Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/616,320A CURRENT FILING DATE: 2003-07-08 NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 21115
                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: PRIMER
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Similarity 81.8%;
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88.9%;
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APPLICANT:

SEIKO

APPLICANT: APPLICANT: APPLICANT:

HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO

APPLICANT:

KEDA, MASATO

AKIO

INVENTION: NOVEL POLYNUCLEOTIDES

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RESULT 10
US-10-369-493-2009
US-10-369-493-2009
; Sequence 20309, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
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US-09-738-626-6285
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CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14080
LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20309
LENGTH: 339
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Best Local Similarity 59.1%;
Matches 13; Conservative
                                 Sequence 6285, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
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CURRENT FILING DATE: 2003-02-28
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TYPE: PRT
APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 MALERNGVTPQQGEVLVTGANG 158
                                                                                                                                                                          164 NDALDEGSLVLVEGTQG 180
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 MIZOGUCHI, HIROSHI
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Pred. No. 5
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Best Local
             SEQ ID NO 67877
LENGTH: 450
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                            Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 78614 SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/207,727
PRIOR TILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
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CURRENT FILING DATE: 2000-12-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITEA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 CURRENT FILING DATE: 2003-02-20
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TYPE: PRT
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                                                                                                                   APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2000-03-21
APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
                                                                                                                                                                                                            APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
                                                                                                        FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/230,347 FILING DATE: 2000-09-09
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Pred. No.
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                                                                                     PALM
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APPLICATION UNMBER: 09/540,167
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
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PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
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TYPE: PRT
; ORGANISM: Escherichia coli
US-10-662-358-1
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                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 39265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39265, Application US/10450763
Publication No. US20050196754A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/10662358
Publication No. US20050037473A1
GENERAL INFORMATION:
APPLICANT: LEE, Sang Yup
APPLICANT: PARK, Si Jae
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Best Local
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CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: KR 10-2003-0025863
PRIOR FILING DATE: 2003-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PROCESS FOR PREPARING POLYHYDROXYALKANOATE EMPLOYING maoC GENE FILE REFERENCE: Q77446
                                            NAME/KEY: DOMAIN
LOCATION: (940)..(982)
COTHER INFORMATION: Aldehyde dehydrogenases glutamic acid proteins domain
OTHER INFORMATION: identified by eMATRIX, accession number BL00687B, p-value=1.675e-
OTHER INFORMATION: 22, raw score of 17.54
                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1096)
                                                                                                                                                                                                               ENGTH: 1096
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7; Conserve
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8; Conserv
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Pred. No.
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Pred. No.
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WESULT 15
US-10-369-493-11253
(Sequence 11253, Application US/10369493)
(Sequence 11253, Application US/10369493)
(Publication No. US20030233675A1)
(Publication No. US20030233675A1)
(Publication No. US20030233675A1)
(Publication No. US20030233675A1)
(Publication No. US20030233675A1)
(Publication No. US2003023A1)
(Publication No. Youngerian States, Steven C. Applicant: Slates, Steven C. Applicant: Goldman, Barry S. APPLICANT: Goldman, Barry S. APPLICANT: Goldman, Barry S. APPLICANT: Chen, Xianfeng
(TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
(PILE REFERENCE: 38-10(52052)B
(CURRENT FILING DATE: 2003-02-2B
(PRIOR APPLICATION NUMBER: US/10/369,493)
(CURRENT FILING DATE: 2003-02-21)
(PRIOR FILING DATE: 2002-02-21)
(PRIOR 
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Search completed: March 11, 2006, 05:16:12 Job time : 102.968 secs
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                                                                                                                                                                                                                                                                                                                                                                                      Query Match 43.9%; Score 47; DB 4; Length 276; Best Local Similarity 55.6%; Pred. No. 57; Matches 10; Conservative 4; Mismatches 4; Indels
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:|:::||::|::|::|
993 VDSGLVPEGAISLICGSAG 1011
                                                                                                                                                                                                5 DNAVLPEGSLVLVTGANG 22
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112 NSAVEMEGSKIVVTGAGG 129
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US-11-087-099-9804

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US-11-082-389-168
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                                         ; TYPE: PRT
, ORGANISM: Corynebacterium glutamicum
US-11-082-389-168
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PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 60/143262
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: US 60/151281
PRIOR APPLICATION NUMBER: US 60/151281
PRIOR APPLICATION NUMBER: US 60/151281
PRIOR APPLICATION NUMBER: US 60/151281
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TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 9804
LENGTH: 174
LENGTH: 174
TYPE: PRT
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Publication No. US20060041961A1
GENERAL INFORMATION:
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                                                                                                         SEQ ID NO 168
LENGTH: 311
Query Match
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PRIOR
PRIOR
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TITLE OF INVENTION: CORVNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
TITLE OF INVENTION: TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/11/082,389
CURRENT FILING DATE: 2005-03-16
                                                                                                                                                     NUMBER OF SEQ ID
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                                                                                                                                                                                                                                                                                                     FILING DATE: 1999-07-01
APPLICATION NUMBER: DE 19931549.3
FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19931550.7
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                                                                                                                                                                                                                                                              FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19932134.5
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APPLICATION NUMBER: DE 19930489.0
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Zelder, Oskar
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o. US20050244935A1
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57.1%;
    41.1%; Score 44;
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Pred. No. 7.5;
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    See File Wrapper or PALM

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    Length 311;
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RESULT 10
US-11-087-099-766
J Sequence 766, Application US/11087099
J Sequence 766, US20060041961A1
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US-10-873-528-162
RESULT 11
US-10-793-626-284
; Sequence 284, Application US/10793626
; Publication No. US20050255478A1
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APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PMC/P211290
CURRENT APPLICATION UNMBER: US/10/873,528
CURRENT FILING DATE: 2004-06-23
PRIOR APPLICATION NUMBER: US/9/769,787
PRIOR APPLICATION NUMBER: GB 9816337.1
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 388
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 162, Application US/10873528 Publication No. US20050276814A1 GENERAL INFORMATION:
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                              Best Local Similarity Matches 9; Conserv
                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 363
TYPE: PRT
                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                  ENGTH: 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.1%;
Local Similarity 47.1%;
es 8; Conservarion
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                                                                                                               348 IAVILNYIMPEGVFVLIT 365
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                                                                                                                                             1 MAKIDNAVLPEGSLVLVT 18
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            Mark S. et al.
                                                                                                                                                                                                41.1%; Score 44;
50.0%; Pred. No.
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Mismatches
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US-11-096-568A-4407
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                                                    Sequence 4406, Application US/11096568A

Publication No. US/20060048240A1

GENERAL INFORMATION:

APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 4407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OP INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT FILING NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 284
LENGTH: 173
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 4406
LENGTH: 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4407, Application US/11096568A PPLIDICATION: US20060048240A1 GENERAL INFORMATION: APPLICANT: Alexandrov, Nickolai et al.
                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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NAME/KEY: misc_feature
LOCATION: (1)..(211)
OTHER INFORMATION: Ceres Seq. ID no. 13637459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 211
TYPE: PRT
ORGANISM: Glycine max
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Local Similarity 31.8%;
1es 7; Conservarium
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Pred. No. 11;
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APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant
FILE REFERENCE: 38-21 (53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 12277
LENGTH: 336
TYPE: PRT
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Best Local Similarity
Watches 9; Conserva
                                                              ; ORGANISM: Thermoplasma acidophilum US-11-087-099-12277
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SOFTWARE: SegWin99, version 1.04
SEQ ID NO 3300
LENGTH: 241
                                                                                                                                                                                                                                     Sequence 12277, Application US/11087099 Publication No. US20060041961A1 GENERAL INFORMATION:
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Publication No. US20
GENERAL INFORMATION
                Query Match
Best Local :
   Matches
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APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)..(228)
OTHER INFORMATION: Ceres Seq. ID no. 13637458
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Similarity
9; Conserv
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              40.2%;
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                Score 43;
Pred. No.
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Pred. No.
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Pred. No.
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                                Length 336;
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AVLPEGSLVLVTGANG

Db 159 AKVKEGQRVLITGAGG 174

Search completed: March 11, 2006, 05:16:52
Job time: 11.873 secs



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